

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: May 24, 2002, 19:15:39 ; Search time 1997.16 Seconds

(without alignments)
3981.696 Million cell updates/sec

Title: W36511
Perfect score: 380
Sequence: 1 GCAGGCACAGCTGCTCC.....ACTATTATTACCAATGAC 380

- Scoring table:
IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1797656 segs, 10463268293 residues
Total number of hits satisfying chosen parameters: 3595312

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :
1: gb_ba:*
2: gb_htg:*
3: gb_in:*
4: gb_om:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
8: gb_pl:*
9: gb_pr:*
10: gb_ro:*
11: gb_sts:*
12: gb_sy:*
13: gb_un:*
14: gb_vl:*
15: em_ba:*
16: em_da:*
17: em_fun:*
18: em_in:*
19: em_mu:*
20: em_om:*
21: em_or:*
22: em_ov:*
23: em_pat:*
24: em_ph:*
25: em_pl:*
26: em_ro:*
27: em_sts:*
28: em_un:*
29: em_vl:*
30: em_htg_hum:*
31: em_htg_inv:*
32: em_htg_other:*
33: em_htgo_inv:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
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1	186.8	49.2	2347	10	MMY14334	Y14334 Mus musculus
2	185.2	48.7	2225	10	AF059251	AF059251 Mus musculus
3	166.4	43.8	183759	2	AL645902	AL645902 Mus musculus
4	166.4	43.8	261031	2	AL645527	AL645527 Mus musculus
5	135.8	35.7	2278	2	AF059250	AF059250 Homo sapi
6	135.8	35.7	2469	6	AR106047	AR106047 Sequence
7	135.8	35.7	2469	6	AF038461	AF038461 Homo sapi
8	121.6	32.0	13652	9	HSA305027	HSA305027 Homo sapi
9	121.6	32.0	159582	2	AC015734	AC015734 Homo sapi
10	102.4	26.9	3636	10	MMN18477	MMN18477 Mus musculus
11	57.4	15.1	4293	9	HSA305021	HSA305021 Homo sapi
12	57.4	15.1	36006	2	AC107913	AC107913 Homo sapi
13	57.4	15.1	159582	2	AC015734	AC015734 Homo sapi
14	55.2	14.5	2136	6	AX304470	AX304470 Sequence
15	55.2	14.5	3082	6	AF182218	AF182218 Homo sapi
16	55.2	14.5	3362	9	HSA269499	HSA269499 Homo sapi
17	50.6	13.3	2536	10	MMALOXE3	MMALOXE3 Mus musculus
18	50.6	13.3	2685	6	AR142985	AR142985 Sequence
19	50.6	13.2	2685	6	HSU78294	HSU78294 Homo sapien
20	50.6	13.2	2942	10	BC015253	BC015253 Mus muscu
21	50.6	13.2	3203	10	MMALOXE3	MMALOXE3 Mus muscu
22	50.6	13.2	3205	6	AR142986	AR142986 Sequence
23	50.6	13.2	3205	10	MMO93277	MMO93277 Mus muscu
24	49.4	13.0	2826	9	HSA305031	HSA305031 Homo sapi
25	49.4	13.0	36006	2	AC107913	AC107913 Homo sapi
26	48.4	12.7	1944	9	AF468052	AF468052 Homo sapi
27	48.4	12.7	2031	9	AF468051	AF468051 Homo sapi
28	48.4	12.7	2111	9	AF468054	AF468054 Homo sapi
29	48.4	12.7	261031	2	AL645527	AL645527 Mus muscu
30	48.4	12.6	2101	4	AF107263	AF107263 Bos tauru
31	45	11.8	2335	9	HDM1212L	M58704 Human 12-11
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34	44	11.6	1809	9	AF149095	AF149095 Human arch
35	44	11.6	1809	9	AF468053	AF468053 Homo sapi
36	42.6	11.2	15898	1	AX024393	AX024393 Sequence
37	42.6	11.2	15898	6	AX024286	AX024286 Sequence
38	42	11.1	173878	2	AC040977	AC040977 Homo sapi
39	42	11.1	220399	2	AC015918	AC015918 Homo sapi
40	37.4	9.8	148159	2	AC084327	AC084327 Mus muscu
41	36.4	9.6	274656	2	AC079538	AC079538 Mus muscu
42	36.2	9.5	120240	2	AC097176	AC097176 Oryza sat
43	35.2	9.3	1819	6	AX098513	AX098513 Sequence
44	35	9.2	1665	4	BT1212L	BT1212L Sequence
45	34.8	9.2	40172	2	AC017567	AC017567 Drosophila

ALIGNMENTS

RESULT 1
LOCUS MMY14334 2347 bp mRNA linear ROD 11-MAR-1999
DEFINITION Mus musculus mRNA for arachidonate 12-lipoxygenase, 12R-type.
ACCESSION Y14334
VERSION Y14334.1 GI:3043452
KEYWORDS 12(R)-lipoxygenase; Alox12B gene; arachidonate 12-lipoxygenase.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 2347)
AUTHORS Kriegl, P.
TITLE Direct Submission
JOURNAL Submitted (28-JUL-1997) P. Kriegl, German Cancer Research Center, Research Program 2, Im Neuenheimer Feld 280, D-69120 Heidelberg, Germany, FRG
REMARK 2 (bases 1 to 2347)
AUTHORS Kriegl, P., Kinzig, A., Heidt, M., Marks, F. and Furstenberger, G.
TITLE cDNA cloning of a 8-lipoxygenase and a novel epidermis-type lipoxygenase from phorbol ester-treated mouse skin
JOURNAL Blochim. Biophys. Acta 1391 (1), 7-12 (1998)

MEDLINE 98186642
 3 (bases 1 to 2347)
 REFERENCE Kriegl, P., Siebert, M., Kinzigt, A., Marks, F., and Fuerstenberger, G.
 AUTHORS Murine 12(R)-lipoxigenase: functional expression, genomic structure
 TITLE and chromosomal localization
 JOURNAL Unpublished
 FEATURES Location/Qualifiers
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 /strain="NMRI"
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 /clone="Y1"
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 /clone_lib="TPA-treated epidermis cDNA in lambda ZAPIT"
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 176..2281
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 /note="12R-type"
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 SYHPPRCRNPENRPMDDGYTPGPIILINIKATFLNSNLRFSVKASFFRLGPM
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 HEVAHLLESHLIGEAFCIALRLNMPCHPLKLIPIHTRYNOINSIGRALLLKGG
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 MERYVTETIITYYYPNDAAVEGDPLOQVOEIFKECILGRESSEPTCLRTIPELEY
 VTMWYTSARHAAVNSQLEYSNMPNPFSSMRNPPMOTKGLTTLQTYMDTLDPVKT
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 BASE COUNT 517 a 688 c 594 g 548 t
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 Best Local Similarity 98.5%; Pred. No. 1.9e-36;
 Matches 199; Conservative 0; Mismatches 2; Indels 1; Gaps 1;
 175 TTTCCTGGGCTAGAGGCTTCGACAGGTGATGTTGGGGGTCTGTGAGCTCAGCT 234
 1542 TGTCCCTGGGCTAGAGGCTTCGACAGGTGATGTTGGGGGTCTGTGAGCTCAGCT 1601
 235 ACAAAAGCCTGCAATTCACAGCACTTTGTGAGCGCGGGGTCCAGAGCTGCTGGGT 294
 1602 ACAAAAGCCTGCAATTCACAGCACTTTGTGAGCGCGGGGTCCAGAGCTGCTGGGT 1661
 295 ATTATTTCCGATGACAGCGCTGGCGGTGTGACGGGATGAGAGGTAAGTACTGAC 354
 1662 ATTATTTCCGATGACAGCGCTGGCGGTGTGACGGGATGAGAGGTAAGTACTGAC 1720
 355 ATCATCACTTATTTATACCAA 376
 1721 ATCATCACTTATTTATACCAA 1742
 RESULT 2
 AF059251 2225 bp mRNA linear ROD 27-NOV-1998
 DEFINITION Mus musculus 12(R)-lipoxygenase (alox) mRNA, complete cds.
 ACCESSION AF059251
 VERSION AF059251.1 GI:3928784
 KEYWORDS

SOURCE house mouse.
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 REFERENCE 1 (bases 1 to 2225)
 AUTHORS Sun, D., McDonnell, M., Chen, X.S., Lakkis, M.M., Li, H., Isaacs, S.N.,
 Elisei, S.H., Patel, P.I., and Funk, C.D.
 TITLE Human 12(R)-lipoxygenase and the mouse ortholog. Molecular cloning,
 expression, and gene chromosomal assignment
 JOURNAL J. Biol. Chem. 273 (50), 33540-33547 (1998)
 REFERENCE 2 (bases 1 to 2225)
 AUTHORS Sun, D. and Funk, C.D.
 TITLE Direct Submission
 JOURNAL Submitted (13-APR-1998) Pharmacology, University of Pennsylvania,
 422 Curie Blvd., Philadelphia, PA 19104, USA
 FEATURES
 source 1..2225
 Location/Qualifiers
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 /strain="B6 SJL/J"
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 /tissue_type="whole body"
 /dev_stage="newborn"
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 /gene="alox"
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 54..2159
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 /db_xref="GI:3928785"
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 SYHPPRCRNPENRPMDDGYTPGPIILINIKATFLNSNLRFSVKASFFRLGPM
 LAFKRLGIDRRKRSKRLKIDINIPATSVSEVYAEHEDSFEFGYGLNIGPL
 IIRCTOIPDKFPPVDEMAVAPLIGSTGLQALEGNTYLDVRIIDGIPVELNGOO
 HHCAAPMLHFGPDGNMPLAIOLSGTPEPDDPIPLPNDEMDLLAKRMVYAEFS
 HEVAHLLESHLIGEAFCIALRLNMPCHPLKLIPIHTRYNOINSIGRALLLKGG
 LSARMSLGLGEGFAOVNVRGSELTYKSLCIPNDYERGVODLPGLYFRDLSLAWYA
 MERYVTETIITYYYPNDAAVEGDPLOQVOEIFKECILGRESSEPTCLRTIPELEY
 VTMWYTSARHAAVNSQLEYSNMPNPFSSMRNPPMOTKGLTTLQTYMDTLDPVKT
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 BASE COUNT 503 a 647 c 565 g 510 t
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 Query Match 48.7%; Score 185.2; DB 10; Length 2225;
 Best Local Similarity 98.0%; Pred. No. 4.8e-36;
 Matches 198; Conservative 0; Mismatches 3; Indels 1; Gaps 1;
 175 TTTCCTGGGCTAGAGGCTTCGACAGGTGATGTTGGGGGTCTGTGAGCTCAGCT 234
 1420 TGTCCCTGGGCTAGAGGCTTCGACAGGTGATGTTGGGGGTCTGTGAGCTCAGCT 1479
 235 ACAAAAGCCTGCAATTCACAGCACTTTGTGAGCGCGGGGTCCAGAGCTGCTGGGT 294
 1480 ACAAAAGCCTGCAATTCACAGCACTTTGTGAGCGCGGGGTCCAGAGCTGCTGGGT 1539
 295 ATTATTTCCGATGACAGCGCTGGCGGTGTGACGGGATGAGAGGTAAGTACTGAC 354
 1540 ATTATTTCCGATGACAGCGCTGGCGGTGTGACGGGATGAGAGGTAAGTACTGAC 1598
 355 ATCATCACTTATTTATACCAA 376
 1599 ATCATCACTTATTTATACCAA 1620

RESULT	3
AL645902	
LOCUS	
DEFINITION	AL645902 183759 bp DNA linear HTG 18-DEC-2001
ACCESSION	Mus musculus chromosome 11 clone RP23-1912, *** SEQUENCING IN PROGRESS ***, in ordered pieces.
VERSION	AL645902
KEYWORDS	AL645902.5 GI:17903578
SOURCE	HTG; HTGS_PHASE2; HTGS_ACTIVERIN; HTGS_DRAFT; HTGS_FULLTOP.
ORGANISM	house mouse. Mus musculus.
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
AUTHORS	1 (sites)
TITLE	Lovell,J.
JOURNAL	Direct Submission
	Submitted (17-DEC-2001) Wellcome Trust Sanger Institute, Hinxton,

COMMENT

Center for Wellcome Trust Sanger Institute
 Center code: SC
 Web site: <http://www.sanger.ac.uk>
 Contact: humquerey@sanger.ac.uk

 Project Information

 Center project name: bml1917

```

Assembly program: XAP4; version 4.5
Sequencing vector: plasmid; L08752; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Consensus quality: 183739 bases at least Q40
Consensus quality: 183750 bases at least Q30
Consensus quality: 183756 bases at least Q20
Insert size: 183759; sum-of-contigs
Insert size: 190781; 2.6% error; agarose-tp
Quality coverage: 17.3x in Q20 bases; sum-of-contigs
Quality coverage: 16.70x in Q20 bases; agarose-tp

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* NOTE: This is a 'working draft' sequence.
* This sequence will be replaced
* by the finished sequence as soon as it is available and
* the accession number will be preserved.

FEATURES

1. .183759

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1. 183759
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Best Local Similarity	99.4%;	Pred. No. 1.1e-31;		
Matches 167;	Conservative	0;	Mismatches 1;	Indels 0

175 TTTCCTGGGCTAGAGGGCTTCGCACAGTGATGGTTCGGGGTCTGTCTGAGCTCACCT 234

Db 182008 TGTCCCTGGGGCTAGAGGGCTTCGCACAGGTGATGCTTCGGGGCTCTGTCTGAGGCTCACCCT 182067

235 ACAGAAAGCCTCTGCATTCCCAACGACTTTGTGGAGCGCGGGGTCCAGGACCTGCCCTGGGT 294

DD 182088 ACAAAGCCTCTGCAATCCCAACGACTTTGTGGAGCGCGGGGTCCAGACCT

Db 182128 ATATTTCGATGACAGCCTGGCGGTGTGTACCGATGAGAGGT 182175

RESULT	4
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LOCUS	261031 bp DNA linear HTG_30-JAN-2007
DEFINITION	Mus musculus chromosome 11 clone RP23-26L6, ***SEQUENCING IN
ACCESSION	AL645527
VERSION	AL645527.12 GI:18250551
KEYWORDS	HTG; HTGS_PHASE1; HTGS_ACTIVEFIN; HTGS_DRAFT; HTGS_FULLTOP.
SOURCE	house mouse.

REFERENCE 1 (sites)
AUTHORS Ashwell, R.
TITLE Direct Submission
JOURNAL Submitted (23-JAN-2002) Wellcome Trust Sanger Institute, Hinxton,

COMMENT

Center: Wellcome Trust Sanger Institute
Center code: SC
Web site: <http://www.sanger.ac.uk>
Contact: humquery@sanger.ac.uk
----- Project Information
Center project name: bm26L6

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Assembly program: XCAP4, version 4.5
Sequencing vector: plasmid, L08752; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Consensus quality: 257475 bases at least Q40
Consensus quality: 258163 bases at least Q30
Consensus quality: 258659 bases at least Q20
Insert size: 259831; sum-of-contigs
Insert size: 221534; 8.6% error; agarose-fp
Quality coverage: 8.13% in Q20 bases; sum-of-contigs
Quality coverage: 9.54% in Q20 bases; agarose-fp

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* NOTE: This is a 'working draft' sequence.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.

FEATURES

source

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1. 4962
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83806. 116048
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Query Match	43.8%;	Score 166.4;	DB 2;	Length 261031;
Best Local Similarity	99.4%;	Pred. No. 1.1e-31;		
Matches 167;	Conservative	0;	Mismatches 1;	Indels 0;
				Gaps 0

QY	175	TTTCCCTGGGGCCAGAGGGCTTCGACACGATGATGTTCCGGGGTCTGCTAGCTACCT	234
Db	82649	TGTCCCTGGGGCCAGAGGGCTTCGACACGATGATGTTCCGGGGTCTGCTAGCTACCT	82708
QY	235	ACAAAGCGCTCGATTCCTCCACGATTTGTGTGACGCGGGGTCCAGACCTGCGTGGT	294
Db	82709	ACAAAGCGCTCGATTCCTCCACGATTTGTGTGACGCGGGGTCCAGACCTGCGTGGT	82768
QY	295	ATTATTCCTCGATGACAGCCTGGCGTGTGTGACGCATGAGAGGT	342
Db	82769	ATTATTCCTCGATGACAGCCTGGCGTGTGTGACGCATGAGAGGT	82816

AF059250	LOCUS	DEFINITION	ACCESSION	VERSION
AF059250	2278 bp	mRNA	linear	PRI 27-NOV-1998
AF059250	Homo sapiens	lipoxxygenase (ALOX12B) mRNA,	complete cds.	
AF059250				
AF059250.1	GI:3928782			

SOURCE ORGANISM	human Homo
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REFERENCE
1 (bases 1 to 22/8)
Sun, D., McDonnell, M., Chen, X. S., Lakkis, M. M., Li, H., Isaacs, S. N., and Park, C. D.

TITLE	Human 12(R)-lipoxygenase and the mouse ortholog. Expression, and gene chromosomal assignment
JOURNAL	J. Biol. Chem. 273 (50), 33540-33547 (1998)

REFERENCE 2 (bases 1 to 2278)
AUTHORS Sun, D. and Funk, C.D.
TITLE Direct Submission
JOURNAL Pharmacology, University of Pennsylvania
Submitted (13-Apr-1998)

FEATURES	Location/Qualifiers
source	1. .2278

gene

5'UTR

CDS

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				Gaps 1

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QY	235	ACAAAAGCCTTCGACATTCGCAACGACTTGTGTGGAGCGGGGGTCCAGGACCTGCCTGGGT	294
Db	1464	ATGACAGCCTTACTACCTCCCAATGACTTGTGTGAGCGTGGGGTCCAGGACCGCTCGGAT	1523
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QY	295	ATTATTTCCGTGATGACAGCTGGCGGGTGTGTACGCCATGGAGAGTACGAGACTAGAG	354
Db	1524	ATTACTACCGCATGACACACTGGGGGTGTGGAAATGCACTGGAAGAATGATGGAC-GGAG	1582
QY	355	ATCATCAGCTATTATTATACG 373	
QY	355	ATCATCAGCTATTATTATACG 373	
Db	1583	ATCATCAGCTATTATTATACG 1601	

RESULT	6		
ARI06047			
LOCUS	2469 bp	DNA	
DEFINITION	Sequence 1 from patent US 6103436.	1linear	PAT 14-FEB-2001

KEYWORDS	
SOURCE	Unknown.
ORGANISM	Unknown.
	Unclassified.

REFERENCE	1 (bases 1 to 213)
AUTHORS	Brash, A.R., Boeglin, W.E. and Kim, R.B.
TITLE	Isolated and purified 18r-lipoxygenase protein and nucleic acids
FEATURES	Patent: US 6103496-A 1 15-AUG-2000;
LOCATION/Qualifiers	

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/organism="unknown"
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ORIGIN

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Best Local Similarity	83.4%	Pred. No. 1e-23		
Matches 106; Conservative	0	Mismatches 32	Indels 1	Gaps 1

QY 175 TTTCCTGCGCCTAGAGGGCTTCCGACAGGTATGTTCCGGGCTCTGCTGAGCTCACCT 234
| | | | | | | | | | | | | | | | | | | | | |
Db 1626 TGTCCCTGGCGGTGGAAGGCTTTTGCTGGGGGTGATGTGCACGGGCTCTGTTCGGAGCTCACCT 1685

Db	1626	TGTCCTGGGCGCGGAAGGCTTGCCTGGGGGTATGTCACGGGCTCTGTGCGAGCTCACT	1685
Qy	235	ACAAAGCCCTCTCATCTTCCCAACGACTTTGTGAGACGGGGGCTCCAGACCTGCTGGGT	294
Db	1686	ATGACACACCTCTACCTCCCAATGACTTTGTGAGACGTGGGGTCCAGACCTGCTGGGAT	1745
Qy	295	ATTATTCCCTGATGACAGCCTGGGGGTGTGATGCGATGAGAGGTACTGACTAGAG	354
Db	1746	ATTACTACCGCGCATGACACTTGGGGGTGTGSAATGCACTGGAAATATGTGAC-GGAG	1804
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175 TTTCCTGGGCTAGAGGGCTTCGACACAGGTGATGGTTGGGGTCTGTCGAGCTCACCT 234

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	/note="exon 4b" /usedin-AJ305026:ALOX12B_mRNA /usedin-AJ305026:ALOX12B_CDS 2869..3187 /gene="ALOX12B"
intron	/note="intron 4b" 3188..3291 /gene="ALOX12B" /number=5
exon	/usedin-AJ305026:ALOX12B_mRNA /usedin-AJ305026:ALOX12B_CDS 3292..3584 /gene="ALOX12B" /number=5
intron	/usedin-AJ305026:ALOX12B_mRNA /usedin-AJ305026:ALOX12B_CDS 3585..3757 /gene="ALOX12B" /number=6
exon	/usedin-AJ305026:ALOX12B_mRNA /usedin-AJ305026:ALOX12B_CDS 3758..3986 /gene="ALOX12B" /number=6
intron	/usedin-AJ305026:ALOX12B_mRNA /usedin-AJ305026:ALOX12B_CDS 3987..4130 /gene="ALOX12B" /number=7
exon	/usedin-AJ305026:ALOX12B_mRNA /usedin-AJ305026:ALOX12B_CDS 4131..6323 /gene="ALOX12B" /number=7
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ORIGIN		
Query Match	33.0%; Score 121.6; DB 9; Length 13652;	
Best Local Similarity	82.7%; Pred. No. 2.7e-20;	
Matches 139; Conservative	0; Mismatches 29; Indels 0; Gaps 0;	
OY 175	TTTCCCTGGGCGCTAGAGGCGTCGCACACAGGTGATGGTTCCGGGCTCTGTACTACCT 234	
Db 7177	TGTCCCTGGGCGTGGAAGCTTTGCTGGGGTGATGGTAGCGGCTCTGCGAGCTCACCT 7236	
OY 235	ACAAAGCCTCGATTGCCAACGACTTGTGGAGCGGCGGCTCCAGSACCCTGCCTGGCT 294	
Db 7237	ATGACAGCCTTACTCTCCCACAATGACTTTGTGGAGCGGTGGGCTCCAGSACCCTGCTGAT 7236	
OY 295	ATTATTTCCGTGATGACAGCCTGGCGGTGTGGTACGCCGATGAGAAGT 342	
Db 7297	ATTACTACCGCATGACAGCTTGGCGGTGTGGAATGCACTGGAGAGT 7244	
RESULT 9		
AC015734	159582 bp DNA linear HTG 13-NOV-2001	
LOCUS	AC015734	
DEFINITION	Homo sapiens clone RP11-ID5, WORKING DRAFT SEQUENCE, 13 unordered pieces.	
ACCESSION	AC015734	
VERSION	AC015734.4 GI:16905302	

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http://lcp.genome.washington.edu/RM/RepeatMasker.html
Center: Whitehead Institute/ MIT Center for Genome Research
Genome Center
Center code: WIR
Web site: http://www-seq.wi.mit.edu
Contact: sequence.submissions@genome.wi.mit.edu
-----
Project Information
Center project name: L1433
Center clone name: L1_D_5
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Summary Statistics
Sequencing vector: M13; M77815; 49% of reads
Sequencing vector: Plasmid; n/a; 51% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.960731
Consensus quality: 155110 bases at least Q40
Consensus quality: 156980 bases at least Q30
Consensus quality: 157688 bases at least Q20
Insert size: 119000; agarose-fp
Insert coverage: 10.7 in Q20 bases; agarose-fp
Quality coverage: 8.1 in Q20 bas.
NOTE: This is a 'working draft' sequence. It currently
consists of 13 contigs. The true order of the pieces
is not known and their order in this sequence record is
arbitrary. Gaps between the contigs are represented as
runs of N, but the exact sizes of the gaps are unknown.
This record will be updated with the finished sequence
as soon as it is available and the accession number will
be preserved.
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1481 1580: gap of 100 bp
1581      2920: contig of 1340 bp in length
2921 3020: gap of 100 bp
3021      6224: contig of 3204 bp in length
6225 6324: gap of 100 bp
6325 13162: contig of 6838 bp in length
13163 13262: gap of 100 bp
13263 19152: contig of 5890 bp in length
19153 19252: gap of 100 bp
19253 73423: contig of 54717 bp in length
73424 73523: gap of 100 bp
73524      81434: contig of 7911 bp in length
81435 81534: gap of 100 bp

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			Gaps 0	
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Db 157766	TGTCCCTGGGCGGTGAGAGGCTTGTCTGGGGGTATGTACGGGCTCTCTCGAGCTCAGCT	157825		
QY 235	ACAAAGCCCTCTGCATTCTCCCAACGACTTTGTGTGAGACGGCGGGGTCCAGAGCTCCCTCGGGT	294		
Db 157826	ATGCACACCCCTCTACCTCCCAATGACTTTGTGTGAGACGGCGGGGTCCAGAGCTCCCTCGGGT	157885		
QY 295	ATTATTCCCTGATGACAGCCTGGCGGGGTGTACGGATCGAGAGCT	342		
Db 157886	ATTACTACCGCGATGACACACTTGGCGGGTGTGGAATGCACCTGAGAGCT	157933		
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LOCUS	MM018477			
DEFINITION	MM018477	3626 bp	DNA	linear
ACCSSION	Y18477	Mus musculus Alox12b gene 5', flanking region.		ROD 14-APR-1999

VERSION	Y18477.1	GI:4586204
KEYWORDS	12(R)-lipoxygenase; Alox12B gene.	
SOURCE	house mouse.	
ORGANISM	Mus musculus.	
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.	
AUTHORS	Krieg, P., Siebert, M., Kinzig, A., Bettenhausen, R., Marks, F. and Furstentberger, G.	
TITLE	Murine 12(R)-lipoxygenase: functional expression, genomic structure and chromosomal localization	
JOURNAL	FEBS Lett. 446 (1), 142-148 (1999)	
MEDLINE	99198730	
REFERENCE	2 (bases 1 to 3626)	
AUTHORS	Krieg, P.	
TITLE	Direct Submission	
JOURNAL	Submitted (26-NOV-1998) P. Krieg, German Cancer Research Center, Research Program 2, Im Neuenheimer Feld 280, D- 69120 Heidelberg, FRG	

FEATURES	Location/Qualifiers
source	1..3626 /organism="Mus musculus" /strain="NMRI" /db_xref="taxon:10090" /chromosome="11" /tissue_type="skin epidermis"
gene	1..3626 /gene="Alox12b"
misc_feature	<1..3626 /gene="Alox12b" /note="5' flanking region"
BASE COUNT	742 a 997 c 723 g 1164 t
ORIGIN	

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Best Local Similarity	99.0%	Pred. No. 2.1e-15		
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			Gaps	0
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Db	3441	AGGCGACACTGTCTCCGGCTCCAGAGCATTCGCGGAGACATGTGTTCCGCGTACTGC	3500	
Qy	63	TCCATCACTGACTGCTCCATCACTCTTCGCTGTGGCTTCCT	106	
Db	3501	TCCATCACTGACTGCTCCATCACTCTTCGCTGTGGCTTCCT	3544	

RESULT 11	4293 bp	DNA	linear	PRI 14-MAR-2001
AJ305021				
CUS				
DEFINITION	HMO:sapiens partial ALOX3 gene for archidonate lipoxygenase 3, exons 5 to 11.			
ACCESSION	AJ305021	GI:1374915		
VERSION	AJ305021.1			
KEYWORDS	ALOX3 gene; archidonate lipoxygenase 3.			
SOURCE	human.			
ORGANISM	Homo sapiens			
REFERENCE	Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.			
AUTHORS	1 (bases 1 to 4293)			
TITLE	Krieg, P., Marks, F., and Fuerstenberger, G.			
JOURNAL	A gene cluster encoding human epidermis-type lipoxygenases at chromosome 1p13.1: Cloning, physical mapping, and expression unpublished			
REFERENCE	2 (bases 1 to 4293)			
AUTHORS	Krieg, P.R.			
TITLE	Direct Submission			
JOURNAL	submitted (18-AUG-2000) Krieg P.R., Research Program on Tumor Cell Regulation, Deutsches Krebsforschungszentrum, Im Neuenheimer Feld 280, Heidelberg, D-69120, GERMANY			
COMMENT	Related sequences: AJ305020 to AJ305031. Overlapping sequence: AC015734.			

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exon		165..268 /gene="ALOXE3" /number=5 /usedin=AJ305020:ALOXE3_mRNA /usedin=AJ305020:ALOXE3_CDS
intron		269..829 /gene="ALOXE3" /number=5 830..1002 /gene="ALOXE3" /number=6 /usedin=AJ305020:ALOXE3_mRNA /usedin=AJ305020:ALOXE3_CDS
exon		1003..1832 /gene="ALOXE3" /number=6 1833..1976 /gene="ALOXE3" /number=7 /usedin=AJ305020:ALOXE3_mRNA /usedin=AJ305020:ALOXE3_CDS
intron		1977..2065 /gene="ALOXE3" /number=7 2066..2269 /gene="ALOXE3" /number=8 /usedin=AJ305020:ALOXE3_mRNA /usedin=AJ305020:ALOXE3_CDS
exon		2270..2358 /gene="ALOXE3" /number=8 2359..2445 /gene="ALOXE3" /number=9 /usedin=AJ305020:ALOXE3_mRNA /usedin=AJ305020:ALOXE3_CDS
intron		2446..3017 /gene="ALOXE3" /number=9 3018..3187 /gene="ALOXE3" /number=10 /usedin=AJ305020:ALOXE3_mRNA /usedin=AJ305020:ALOXE3_CDS
exon		3188..3771 /gene="ALOXE3" /number=10 3772..3893 /gene="ALOXE3" /number=11 /usedin=AJ305020:ALOXE3_mRNA /usedin=AJ305020:ALOXE3_CDS
intron		3894..>4293 /gene="ALOXE3" /number=11
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ORIGIN		

Query Match 15.1%; Score 57.4; DB 9;
Best Local Similarity 58.5%; Pred. No. 0.00035;
Length 4293

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DEFINITION	Homo sapiens chromosome 17 clone CTD-3051C7 map 17, LOW-PASS SEQUENCE SAMPLING.
VERSION	AC107913
VERSION	AC107913.1 GI:18308639
KEYWORDS	HTG; HTGS_PHASEO.
SOURCE	human.
ORGANISM	Homo sapiens

Anderson, S., Barna, N., Bastien, V., Boguslavsky, L., Boukhalter, B., Brown, A., Camarata, J., Campodiano, A., Chang, J.Y., Chazaro, B., Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cook, A., Cooke, P., Deakellano, K., Dewar, K., Diaz, J.S., Dodge, S., Fero, S., Ferreira, P., Fitzhugh, W., Gage, D., Galagan, J., Gaidyna, S., Glinde, S., Gord, S., Goyette, M., Graham, L., Grand-Pierre, N., Hagos, B., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C., Kamat, A., Karatas, A., Kells, C., LaRoque, K., Lamazares, R., Landers, T., Lehoczyk, J., Levine, R., Liu, G., Maclean, C., Macdonald, P., Major, J., Marquis, N., Matthews, C., McCarthy, M., Mcowan, P., Mckernan, K., Meldrum, J., Menelus, L., Milnova, T., Mienga, V., Murphy, T., Naylor, J., Nguyen, C., Nicol, R., Notbu, C., Notman, C. H., O'Connor, T., O'Donnell, P., O'Neill, D., Oliver, J., Peterson, K., Phunkhang, P., PIERRE, N., Pollara, V., Raymond, C., Retta, R., Ribback, M., Riley, R., Risse, C., Rogov, P., Roman, J., Rosetti, M., Roy, A., Santos, R., Schauer, S., Schuppback, R., Seaman, S., Severs, P., Spencer, B., Stange-Thomann, N., Stojanovic, N., Stray, N., Subramanian, A., Talamas, J., Testaye, S., Theodore, J., Topham, K., Travers, M., Travis, N., Triggillo, J., Vassiliev, H., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W. D., Young, G., Zalnoun, J., Zembek, L., Zimmer, A. and Zody, M.

Smut, A.F.A. & Green, P (1996-1997)
 http://ftp.genome.washington.edu/BW/RepeatMasker.html
 ----- Genome Center
 Center: Whitehead Institute/ MIT Center for Genome Research
 Center code: WIBR
 Web site: http://www-seq.wi.mit.edu
 Contact: sequence.submissions@genome.wi.mit.edu
 ----- Project Information
 Center project name: L23044
 Center clone name: J051_C_7

* activity. Low-pass sequence sampling is useful for			
* identifying clones that may be gene-rich and allows			
* overlap relationships among clones to be deduced.			
* However, it should not be assumed that this clone			
* will be sequenced to completion. In the event that			
* the record is updated, the accession number will			
* be preserved.			
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*	663	762:	gap of 100 bp
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*	2299	2964:	contig of 666 bp in length
*	2965	3064:	gap of 100 bp
*	3065	3731:	contig of 667 bp in length
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*	3832	4534:	contig of 703 bp in length
*	4535	4634:	gap of 100 bp
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 * 27377 27476: gap of 100 bp in length
 * 27477 28185: contig of 709 bp in length
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FEATURES
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BASE COUNT
 ORIGIN
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Query Match 15.1%; Score 57.4; DB 2; Length 36006;
 Best Local Similarity 58.5%; Pred. No. 0.00025;
 Matches 100; Conservative 0; Mismatches 71; Indels 0; Gaps 0;

Oy 177 TCCTGGGCGCTAGAGGCTTGGACAGGTGATGGGTCTGTGAGCTCAGCTAC 236
 Db 34071 TCCATCGGCGAGGAGGAGGCTATCTACTCTAGACAGCGGCGCCCTCCTCAGCTAC 34012
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 Db 34011 ACCATTTCTCTCTCCGAGACGCTCGGCGGCGGCGGCTCTGCTATCCCACTAC 33952
 Db 297 TATTTCCGTGATGACAGCGCTGCGGTGATGACGATGAGAGGTGATG 347
 Db 33951 CACTACCGAGAGGAGGCGCTGAGATCTGGGCGGCGCATTTAGAGGTGCGAG 33901

RESULT 13
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 LOCUS Homo sapiens clone RP11-1D5, WORKING DRAFT SEQUENCE, 13 unordered
 DEFINITION pieces.
 ACCESSION AC015734
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 KEYWORDS HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_FULLTOP.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 159582)
 AUTHORS Birren,B., Linton,L., Nusbaum,C. and Lander,E.
 TITLE Homo sapiens, clone RP11-1D5
 JOURNAL Unpublished
 REFERENCE 2 (bases 1 to 159582)
 AUTHORS Birren,B., Linton,L., Nusbaum,C., Lander,E., Allen,N., Anderson,M.,
 Baldwin,J., Batra,N., Beckerly,R., Boguslavsky,L., Boukhgalter,B.,

TITLE
 JOURNAL
 COMMENT

Brown,A., Castle,A., Colangelo,M., Collins,S., Collimore,A.,
 Cooke,P., Dearlano,K., Dewar,K., Domino,M., Donelan,L., Doyle,M.,
 Ferreira,P., Fitzhugh,W., Forrest,C., Funke,R., Gage,D.,
 Galagan,J., Gardyna,S., Grant,G., Hago,B., Heaford,A., Horton,L.,
 Howland,J.C., Johnson,R., Jones,C., Kann,L., Karatas,A., Klein,J.,
 Lehoczy,J., Lien,C., Locke,K., Macdonald,P., Marquis,N.,
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 Morrow,J., Naylor,J., Norman,C.H., O'Connor,T., O'Donnell,P.,
 Peterson,K., Pollara,V., Riley,R., Roy,A., Santos,R., Severy,P.,
 Stange-Thomann,N., Stojanovic,N., Subramanian,A., Talamas,J.,
 Testaie,S., Tirrell,A., Vassiliev,H., Vo,A., Wheeler,J., Wu,X.,
 Wyman,D., Ye,W.J., Zimmer,A. and Zody,M.
 Direct Submission
 Submitted (17-NOV-1999) Whitehead Institute/MIT Center for Genome
 Research, 320 Charles Street, Cambridge, MA 02141, USA
 On Nov 13, 2001 this sequence version replaced g1:7543748.
 All repeats were identified using RepeatMasker:
 Smit,A.F.A. & Green, P. (1996-1997)
 http://ftp.genome.washington.edu/RM/RepeatMasker.html

Center: Whitehead Institute/ MIT Center for Genome Research
 Center code: WIBR
 Web site: http://www-seq.wi.mit.edu
 Contact: sequence_submissions@genome.wi.mit.edu
 Project Information
 Center project name: 14433
 Center clone name: 1.D-5

Summary Statistics
 Sequencing vector: M13; W77815; 49% of reads
 Sequencing vector: Plasmid; n/a; 51% of reads
 Chemistry: Dye-terminator Big Dye; 100% of reads
 Assembly program: Phrap; version 0.960731
 Consensus quality: 155110 bases at least Q40
 Consensus quality: 156980 bases at least Q30
 Consensus quality: 157688 bases at least Q20
 Insert size: 119000; agarose-fp
 Insert size: 158382; sum-of-contigs
 Quality coverage: 10.7 in Q20 bases; agarose-fp
 Quality coverage: 8.1 in Q20 bas.

NOTE: This is a 'working draft' sequence. It currently
 consists of 13 contigs. The true order of the pieces
 is not known and their order in this sequence record is
 arbitrary. Gaps between the contigs are represented as
 runs of N, but the exact sizes of the gaps are unknown.
 This record will be updated with the finished sequence
 as soon as it is available and the accession number will
 be preserved.

1 1480: contig of 1480 bp in length
 * 1481 1580: gap of 100 bp
 * 1581 2920: contig of 1340 bp in length
 * 2921 3020: gap of 100 bp
 * 3021 6224: contig of 3204 bp in length
 * 6225 6324: gap of 100 bp
 * 6325 13162: contig of 6838 bp in length
 * 13163 13262: gap of 100 bp
 * 13263 19152: contig of 5890 bp in length
 * 19153 19252: gap of 100 bp
 * 19253 73423: contig of 54171 bp in length
 * 73424 73523: gap of 100 bp
 * 73524 81434: contig of 7911 bp in length
 * 81435 81534: gap of 100 bp
 * 81535 91266: contig of 9732 bp in length
 * 91267 91366: gap of 100 bp
 * 91367 104881: contig of 13515 bp in length
 * 104882 104981: gap of 100 bp
 * 104982 117370: contig of 12389 bp in length
 * 117371 117470: gap of 100 bp
 * 117471 133737: contig of 16267 bp in length
 * 133738 133837: gap of 100 bp
 * 133838 155551: contig of 21714 bp in length
 * 155552 155651: gap of 100 bp
 * 155652 159582: contig of 3931 bp in length.
 Location/Qualifiers

FEATURES

Query Match	15.1%	Score 57.4	DB 2	Length 159582
Best Local Similarity	58.5%	Pred. No. 0.00019		
Matches 100	Conservative	0	Mismatches 71	Indels 0
				Gaps 0
Db 177	TCCTGGGCGCTTAGAGGGCTTGCCACAGGTGATGTGCGGGGTCTGTCTGAGCTCACCTAC	236		
Db 50049	TCCTATTCGGGAGGCGCAAGGGCTCATCTACCTCAGACACGAGGGCTGGCCACTTCACCTAC	49990		
Db 237	AAAAGCCTCTGCATTCCTCCCAACGACTTTGTGAGCGCGGGGTCCAGACACTCGCTGGGTAT	296		
Db 49989	ACCAATTTCTGCGCTTCCGAGACGCTGGGGGGCGGCGCTGTGGCTATCCCAACTAC	49930		
Db 49929	CACCTACGAGACGACGGGCTTAAGATCTGGGCGGCGCATTTGAGAGGTGGCAG	49879		
RESULT 14				
LOCUS	AX304470	2136 bp	DNA	Linear
DEFINITION	Sequence 8 from Patent WO0185956.			
ACCESSION	AX304470			
VERSION	AX304470.1	GI:17383841		
KEYWORDS	human.			
SOURCE	Homo sapiens			
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidi; Homo.			
REFERENCE	1 (stiles)			
AUTHORS	Das,D., Reddy,R., Yao,M.G., Nguyen,D.B., Lu,Y., Tribouley,C.M., Yee,H., Khan,F.A., Gandhi,A.R., Au-Yang,U., Lal,P., Kearney,L., Elliott,V.S., Ding,L. and Thirionon,M.			
TITLE	Lipid metabolism enzymes			
JOURNAL	Patent: WO 0185956-A 8 15-NOV-2001;			

gene
CDS

/organism="Homo sapiens"
/db_xref="taxon:9606"
1..3082
/gene="ALOXE3"
202..2337
/gene="ALOXE3"
/note="similar to mouse ALOXE3"
/codon_start=1
/product="epidermal lipoygenase"
/protein_id="AAG16899.1"
/db_xref="GI:10441004"
/translation="MAVYRLCVTGYPLRAGTLDNISVTLVGTGSGSPKRLDMRGD
FAGSVOKTKVRCSTALGELLTLVHKERAFKRCWSVCRLCVTEPDSVSHPFY
QWEGCVTELRPGTARTICQDSILPLDLHRTBELRABECYSRKTYAPFCMVVYN
SEQEMESDKRFALTKTTTCVDQDSSGNNRIPELPMKIDIPSLATMEPNVRSATGI
SLFNAIPASLGMKRLGLLDRKGSYKRLDMQNIEMWCHRTFTTKVYTEHNCEDEHFGY
OYINGNCPYMLACISLPSKIPYTNMDVAPILGQDPCITQTELRGMIPLADYVITIAEA
PHNGCNROOYVAPRCLMLSPQCALVPEALDIOSTPGHDSFTPLPTGSEMDMLAK
TWVRNSEPLVHENNHTELCTHLCEAFAMATYLNQDPLCHPIYKLLPHRYTYLQNTVI

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: May 24, 2002, 18:05:53 ; Search time 1935.21 Seconds

(without alignments)
2650.277 Million cell updates/sec

Title: W36511
Perfect score: 380
Sequence: 1 GCAAGCAGCAGCTCTCC.....ACTTATTATTCACCAATGAC 380

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 13736207 segs, 6748477542 residues
Total number of hits satisfying chosen parameters: 27472414

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
EST:
1: em_estlba:*
2: em_estlhum:*
3: em_estlin:*
4: em_estlmu:*
5: em_estlsv:*
6: em_estlpl:*
7: em_estlro:*
8: em_estlhc:*
9: gb_estl:*
10: gb_estl2:*
11: gb_hlc:*
12: gb_gss:*
13: em_gss_hum:*
14: em_gss_inv:*
15: em_gss_pln:*
16: em_gss_vrtl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	380	100.0	380	10 W36511	W36511 mb76f09.r1
2	185.2	48.7	462	10 AA760573	AA760573 vv78h03.r
3	174.8	46.0	361	10 W10508	W10508 ma40f06.r1
4	151.4	39.8	553	10 BF466248	BF466248 UT-M-CGCP
5	131.6	34.6	645	10 BG436629	BG436629 602489125
6	121.6	32.0	425	10 BG946103	BG946103 MR3-KT005
7	115	30.3	499	9 AM488090	AM488090 UI-M-BH3-
8	114.6	30.2	818	10 BG698713	BG698713 602703088
9	100.4	26.4	795	10 B1667266	B1667266 60392520
10	97	25.5	100	10 W18678	W18678 mp98f01.r1
11	93.4	24.6	518	9 AT788059	AT788059 u116g08.y
12	89.8	23.6	214	10 W11802	W11802 mb22h02.r1
13	88	23.2	214	9 BB587762	BB587762 BB587762
14	80.4	21.2	257	9 AA038641	AA038641 m194a06.r
15	80.4	21.2	449	9 AT385442	AT385442 m194a06.y
16	75	17.7	277	10 BE715737	BE715737 CM4-HT075
17	66.4	17.5	445	10 BF464406	BF464406 UT-M-CGCP

C	18	55.4	14.6	433	9	AN047244	UT-M-BH1-
	19	52.6	13.8	479	9	A0243940	A0243940
	20	50	13.2	605	10	B1489877	B1489877 603031627
	21	50	13.2	761	10	BG740246	BG740246 602630664
	22	50	13.2	833	10	BG675395	BG675395 602621712
	23	50	13.2	840	10	BG740579	BG740579 602633094
	24	50	13.2	845	10	BG740763	BG740763 602632735
	25	50	13.2	876	10	BG674800	BG674800 602620931
	26	50	13.2	892	10	BG743633	BG743633 602633993
	27	50	13.2	893	10	BG741964	BG741964 602633405
	28	49.4	13.0	628	9	BB378807	BB378807
	29	48.4	13.0	669	12	AG090131	AG090131 Pen trogl
	30	48.8	12.8	843	10	BG739709	BG739709 602630403
	31	48.8	12.8	863	10	BG696031	BG696031 602658180
	32	48.4	12.7	556	12	BH088160	BH088160 RPCI-24-3
	33	47.4	12.5	361	9	AT324883	AT324883 m194a06.x
	34	45	11.8	865	10	BG742611	BG742611 602633205
	35	43.6	11.5	550	12	A0594148	A0594148 HS_5334_A
	36	40.6	10.7	350	9	AM158910	AM158910 z49a08.x
	37	40	10.5	813	10	BF674881	BF674881 602136749
	38	38.4	10.1	832	10	BG698185	BG698185 602660087
	39	37.8	9.9	765	10	BG934596	BG934596 SK1-0908
	40	36.6	9.6	415	10	BE483723	BE483723 170000 BA
	41	36.4	9.6	841	10	BG483904	BG483904 602504481
	42	35.6	9.4	446	9	BB732451	BB732451
	43	35.4	9.3	414	10	BE982417	BE982417 UT-M-CGCP
	44	35.4	9.3	697	10	BG739860	BG739860 602630592
	45	35.2	9.3	429	9	AV608986	AV608986

ALIGNMENTS

RESULT 1
LOCUS W36511 380 bp mRNA linear EST 11-SEP-1996
DEFINITION mb76f09.r1 Soares mouse p3NMf19.5 Mus musculus cDNA clone
IMAGE:335369 5' similar to SW:10X2_HUMAN P18054 ARACHIDONATE
12-LIPOXYGENASE ; mRNA sequence.

ACCESSION W36511 GI:1318416

VERSION W36511.1 GI:1318416

KEYWORDS EST.

SOURCE house mouse.

ORGANISM Mus musculus

REFERENCE
1 (bases 1 to 380)
Marrin,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,D., Morris,M.,
Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
Waterston,R.

TITLE The WashU-HMI Mouse EST Project
JOURNAL Unpublished (1996)
COMMENT Contact: Marra M/Mouse EST Project
WashU-HMI Mouse EST Project
Washington University School of Medicine
444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810

FEATURES
source
Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LML; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
MGI:218769
Possible reversed clone: similarly on wrong strand
Seq primer: ETPRimer
High quality sequence stop: 332.
Location/Qualifiers
1..380
/organism="Mus musculus"
/db_xref="taxon:10090"
/clone="IMAGE:335369"
/clone_lib="Soares mouse p3NMf19.5"

JOURNAL Unpublished (1996)
COMMENT Contact: Maria M/Mouse EST Project
WashU-HMHT Mouse EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: mouseest@wustl.edu
This clone is available royalty-free through LBNL; contact the
IMAGE Consortium (info@image.lbnl.gov) for further information.
MGI: 203803

Seq primer: mod.REGA+ET
High quality sequence stop: 337.
Location/Qualifiers
1. 361
/organism="Mus musculus"
/db_xref="taxon:10090"
/clone="IMAGE:313187"
/dev_stage="19.5 dpc total fetus"
/lab_host="DH10B (ampicillin resistant)"
/note="Vector: pT73D (Pharmacia) with a modified
polylinker, Site_1: Not I, Site_2: Eco RI; 1st strand cDNA
was primed with a Not I - oligo(dT) primer [5'
TGTACCAATCTGAGAGTGGAGCGGCGGATTTTCTTTTCTTTT 3']
double-stranded cDNA was size selected, ligated to Eco RI
adapters (Pharmacia), digested with Not I and cloned into
the Not I and Eco RI sites of a modified pT73 vector
(Pharmacia). Library went through one round of
normalization to a Col = 5. Library constructed by Bento
Soares and M.Falima Bonaldo. RNA was kindly provided by
Dr. Minoru Ko (Wayne State University)."

BASE COUNT 79 a 92 c 108 g 82 t
ORIGIN

Query Match 46.0%; Score 174.8; DB 10; Length 361;
Best Local Similarity 98.0%; Pred. No. 8.9e-41;
Matches 198; Conservative 0; Mismatches 2; Indels 2; Gaps 2;

Y 175 TTTCCTGGGCTAGAGGCTTGCACAGGTGATGGTGGGCTGTGAGCTCAGCT 234
D 7 TGTCCCTGGGCTTGA-GGCTTGCACAGGTGATGGTGGGCTGTGAGCTCAGCT 65
Y 235 ACAAAAGCCTCTGCATTCGCCAGAGCTTTGTGAGCGGGGTCAGAGCTGCTGGGT 294
D 66 ACAAAAGCCTCTGCATTCGCCAGAGCTTTGTGAGCGGGGTCAGAGCTGCTGGGT 125
Y 295 ATTTATTTCCGTGATGACAGCTGGCGGTGTGATGCGGATGAGAGCTGCTGAGAG 354
D 126 ATTTATTTCCGTGATGACAGCTGGCGGTGTGATGCGGATGAGAGCTGCTGAGAG 184
Y 355 ATCATCACTATTATTACCAAA 376
D 185 ATCATCACTATTATTACCAAA 206

RESULT 4 553 bp mRNA linear EST 04-DEC-2000
LOCUS BF466248/c
DEFINITION UI-M-CGOp-bqv-c-02-0-UI.s1 NIH_BMAP_Ret4_S2 Mus musculus cDNA clone
VERSION UI-M-CGOp-bqv-c-02-0-UI 3', mRNA sequence.
ACCESSION BF466248
KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 553)
AUTHORS Bonaldo,M.F., Lennon,G. and Soares,M.B.
TITLE Normalization and subtraction: two approaches to facilitate gene
discovery

JOURNAL Genome Res. 6 (9), 791-806 (1996)
MEDLINE 97044477
COMMENT Contact: Chin, H
National Institute of Mental Health
6001 Executive Blvd. Room 7N-7190, MSC 9643, Bethesda, MD
20892-9643, USA
Tel: 301 443 1706
Fax: 301 443 9890
Email: MEST@mail.nih.gov
Oligo-dT track not found, Not I site shown in beginning of sequence
is likely internal to the message. cDNA Library Preparation: M.B.
Soares Lab Clone distribution: Researchers may obtain BMAP cDNA
clones from RESEARCH GENERICS. It should be noted that Bento Soares
is generating a small number of additional specialized
non-redundant arrays of BMAP cDNAs whose availability will be
considered under appropriate and limited collaborative arrangements
Seq primer: M13 Forward
PolyA-No.

FEATURES
source
1. 553
Location/Qualifiers
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UI-M-CGOp-bqv-c-02-0-UI"
/clone_lib="NIH_BMAP_Ret4_S2"
/lab_host="DH10B (Life Technologies)"
/note="Vector: pT73D-Pac (Pharmacia) with a modified
polylinker, Site_1: Not I, Site_2: Eco RI; The
NIH_BMAP_Ret4_S2 library is a subtracted library,
ultimately derived from mouse retina tissue libraries at
various stages of development. For a detailed description
of the library from which this clone was derived, please
visit our web site at brainest.eng.uiowa.edu.
TAG_SEQ=None found"

BASE COUNT 121 a 156 c 152 g 123 t 1 others
ORIGIN

Query Match 39.8%; Score 151.4; DB 10; Length 553;
Best Local Similarity 97.9%; Pred. No. 8.1e-34;
Matches 185; Conservative 0; Mismatches 1; Indels 3; Gaps 3;

Y 188 AAGAGCCTTGCACAGGTGATGGTGGGCTGTGAGCTCAGCTCAAAAGCCTCTG 247
D 553 AAGAGCCTTGCACAGGTGAT-GTTCGGGCTGTGAGCTCAGCTCAAAAGCCTCTG 495
Y 248 CATTCCCAAGCACTTTGTGAGAGCGGGGTCAGAGCTGCTGGCTATTATTCGCGA 307
D 494 CATTCCCAAGCACTTTGTGAGAGCGGGGTCAGAGCTGCTGGCTATTATTCGCGA 436
Y 308 TGACAGCTCGGCGGTGTGATGCGGATGAGAGCTGATGATCACTATTATT 367
D 435 TGACAGCTCGGCGGTGTGATGCGGATGAGAGCTGATGATCACTATTATT 377
Y 368 ATTACCAAA 376
D 376 ATTACCAAA 368

RESULT 5 645 bp mRNA linear EST 14-MAR-2001
LOCUS BG436629
DEFINITION 602489125P1 NIH_MGC_18 Homo sapiens cDNA clone IMAGE:4620966 5',
mRNA sequence.
ACCESSION BG436629
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 645)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.

TITLE	National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL	Unpublished (1999)
COMMENT	Contact: Robert Strausberg, Ph.D. Robert.Strausberg@nih.gov

BASE COUNT	122 a	201 c	190 g	132 t
ORIGIN				

Query Match	34.6%	Score	131.6	DB	10	Length	645
Best Local Similarity	80.6%	Pred	No. 5.7e-28				
Matches	166	Conservative	0	Mismatches	39	Indels	1
						Gaps	1

RESULT	6	425 bp	mRNA	linear	EST 11-JUN-2001
LOCUS	BG946103				
DEFINITION	MR3-KT0050-080101-001-c03	KT0050	Homo sapiens	CDNA,	mRNA sequence.
ACCESSION	BG946103				
VERSION	BG946103.1	GI:14345474			
KEYWORDS	EST.				
SOURCE	human.				
ORGANISM	Homo sapiens				

sequence tags
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000).
MEDLINE 20202663
COMMENT Contact: Simpson A.J.G.

BASE COUNT	77 a	99 c	155 g	94 t
ORIGIN				

Query Match	32.0%	Score 121.6;	DB 10;	Length 425;
Best Local Similarity	82.7%	Pred. No. 4.1e-25;		
Matches 139; Conservative	0;	Mismatches 29;	Indels 0;	Gaps 0;

RESULT	7				
LOCUS	AW488090/c				
DEFINITION	AW488090	499 bp	mRNA	linear	EST 24-FEB-2000
ACCESSION	U1-M-BH3-arr-e-11-0-U1	s1	NIH_BMP_M_S4	Mus musculus	CDNA clone
VERSION	U1-M-BH3-arr-e-11-0-U1	3'			mRNA sequence.
KEYWORDS	AW488090.1	GI:7058360			
EST					

REFERENCE	1 (bases 1 to 499)
AUTHORS	Bonaldi,M.F., Lennon,G. and Soares,M.B.
TITLE	Normalization and subtraction: two approaches to facilitate gene discovery
JOURNAL	Genome Res. 6 (9), 791-806 (1996)
MEDLINE	97044477
COMMENT	Contact: Chin, H

20892-9643, USA
Tel: 301 443 1706
Fax: 301 443 9890
Email: mestr@mail.nih.gov
Oligo-dT track not found. Not I site shown in beginning of sequence is likely internal to the message. cDNA Library Preparation: M.B. Soares Lab Clone Distribution: Researchers may obtain BMAP cDNA clones from RESEARCH GENETICS. It should be noted that Benito Soares is generating a small number of additional specialized non-redundant arrays of BMAP cDNAs whose availability will be considered under appropriate and limited collaborative arrangements
Seq primer: M13 Forward
POLY-A-No.

FEATURES

Source Location/Qualifiers
1..499
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone_lib="NIH-BMAP-M_S4"
/dev_stage="27-32 days"
/lab_host="DH10B (Life Technologies)"
/note="Vector: pT73D-Pac (Pharmacia) with a modified polylinker. Site 1: Not I; Site 2: Eco RI; The NIH-BMAP-M_S4 library is a subtracted library of a series, ultimately derived from a mixture of individually tagged normalized libraries from ten regions of the mouse brain (cerebellum, brain stems, olfactory bulbs, hypothalamus, cortex, amygdala, basal ganglia, pineal gland, striatum, hippocampus) after a series of subtractions to reduce the representation of cDNAs from which ESTs had already been generated. The following serially subtracted libraries were generated in this process: NIH-BMAP-M_S3.1, NIH-BMAP-M_S3.2, NIH-BMAP-M_S3.1, NIH-BMAP-M_S2, NIH-BMAP-M_S1. The subtracted library (NIH-BMAP-M_S4) was constructed as follows: PCR amplified cDNA inserts from NIH-BMAP-M_S3.3, NIH-BMAP-M_S3.2, and NIH-BMAP-M_S3.1 clones from which 3' ESTs had been derived was used as a driver in a hybridization with a pool of the NIH-BMAP-M_S3.3, NIH-BMAP-M_S3.2, and NIH-BMAP-M_S3.1 libraries in the form of single-stranded circles. The remaining single-stranded circles (subtracted library) was purified by hydroxyapatite column chromatography, converted to double-stranded circles and electroporated into DH10B bacteria (Life Technologies) to generate the NIH-BMAP-M_S4 library. This procedure has been previously described (Bonaldo, Lennon and Soares, Genome Research 6:791-806, 1996)
TAG_LIB=NIH-BMAP-M_S4
TAG_TISSUE=basal-ganglia
TAG_SEQ=TCGTAC"

BASE COUNT 107 a 139 c 142 g 111 t
ORIGIN

Query Match 30.3%; Score 115; DB 9; Length 499;
Best Local Similarity 95.6%; Pred. No. 3.8e-23;
Matches 129; Conservative 0; Mismatches 5; Indels 1; Gaps 1;

242 CCTGTGATTCACAGACGCTTTGTGAGCGCGGGGTCACAGACCTGCTGGTATTATT 301
|||||
499 CCTGTGATTCACAGACGCTTTGTGAGCGCGGGGTCACAGACCTGCTGGTATTATT 440
302 CCGGATGACAGCGCTGGCGGTGTGAGCGGATGAGAGGTAGTACTGATGACATCATCA 361
|||||
439 CCGGATGACAGCGCTGGCGGTGTGAGCGGATGAGAGGTAGTACTGATGACATCATCA 381
362 CTATATTATACCAA 376
|||||
380 CTATATTATACCAA 366

RESULT 8

BG698713 818 bp mRNA linear EST 07-MAY-2001
LOCUS 602703086F1 NCL_CGAP_Skn3 Homo sapiens cDNA clone IMAGE:4800620 5',
DEFINITION mRNA sequence.
ACCESSION BG698713
VERSION BG698713.1 GI:13966275
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE 1 (bases 1 to 818)
NIH-MGC <http://mgs.nci.nih.gov/>.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgaps@mail.nih.gov
Tissue Procurement: James Cleaver, M.D.
cDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
Plate: LHAM10691 row: 0 column: 21
High quality sequence stop: 779.

FEATURES

Source Location/Qualifiers
1..818
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="IMAGE:4800620"
/clone_lib="NCL_CGAP_Skn3"
/lab_host="DH10B (T1 phage-resistant)"
/note="Organ: skin; Vector: pCMV-Sport6; Site 1: NotI; Site 2: SalI; Cloned unidirectionally. Primer: Oligo dT. Average insert size 1.5kb. Library constructed by Life Technologies. Note: this is a NCL_CGAP Library."
BASE COUNT 158 a 250 c 237 g 173 t
ORIGIN

Query Match 30.2%; Score 114.6; DB 10; Length 818;
Best Local Similarity 75.6%; Pred. No. 6.3e-23;
Matches 155; Conservative 0; Mismatches 49; Indels 1; Gaps 1;

175 TTTCCTGGGCGCTAGAGGGGTTGGACAGTATGTTGGGCTGTGTGACCTACCT 234
|||||
417 TGTCCCTGGGCGCTGGAAGGCTTTGCTGGGATGATGAGGCTGTGAGCTACCT 476
235 ACAAAGCCTTGATTCGCCAAG-ACCTTTGAGAGCGGGGTCACAGACCTGCTGGG 293
|||||
477 ATGACAGCCTTACCTCCCAATGACACTTTGTGAGCGGTGGGCTCAGACCTGCTGGA 536
294 TATTATTTCCGATGACAGCGCTGGCGGTGTGAGCGGATGAGAGGTAGTACTGACTAGA 533
|||||
537 TATTACTACCGGATGACAGCTTGGCGGTGTGGAATGACGTTGAGAAATATATGACGGA 596
354 GATCATCACTTATTATTACCAATG 378
|||||
597 GATCATCACTTATTATTACCGGAG 621

RESULT 9
B1667266 795 bp mRNA linear EST 12-SEP-2001
LOCUS 603292520F1 NIH_MGC_96 Homo sapiens cDNA clone IMAGE:5311901 5',
DEFINITION mRNA sequence.
ACCESSION B1667266
VERSION B1667266.1 GI:15581499
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

TITLE The WashU-NCI Mouse EST Project 1999
JOURNAL Unpublished (1999)
COMMENT Contact: Marra M/MashU-NCI Mouse EST Project 1999
 Washington University School of Medicine
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
 Tel: 314 286 1800
 Fax: 314 286 1810
 Email: mouseest@wustl.edu
 This clone is available royalty-free through LNL; contact the
 IMAGE Consortium (infoimage.lnl.gov) for further information.
 MGI:995458
 Seg primer: custom primer used
 High quality sequence stop: 518.
FEATURES
 Source
 1..518
 /organism="Mus musculus"
 /strain="C57BL"
 /db_xref="taxon:10090"
 /clone="IMAGE:2087774"
 /clone_lib="Sugano mouse embryo mewa"
 /dev_stage="embryo, 14 dpc"
 /lab_host="DH10B"
 /note="Vector: pME18S-FL3; Site 1: DraIII (CACTGCTG);
 Site 2: DraIII (CACCAGTGG); 1st strand cDNA was primed
 with an oligo(dT) primer [ATGTGGCTTTTCTTTTCTTTT];
 double-stranded cDNA was ligated to a DraIII adaptor
 [CTGTGGCTCTAGG], digested and cloned into distinct DraIII
 sites of the pME18S-FL3 vector (5' site CACTGCTG, 3' site
 CACCAGTGG). XhoI should be used to isolate the cDNA
 insert. Size selection was performed to exclude fragments
 <1.5kb. Library constructed by Dr. Sumio Sugano
 (University of Tokyo Institute of Medical Science).
 Custom primers for sequencing: 5' end primer
 CTCTGCTCTAAAGCTGCG and 3' end primer
 CGACCTGCACCTCGACACA."

BASE COUNT 98 a 151 c 142 g 127 t
ORIGIN

Query Match 24.6%; Score 93.4; DB 9; Length 518;
 Best Local Similarity 98.9%; Pred. No. 8.7e-17;
 Matches 94; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 12 GCTGCTCCGCGTCAGAGCATTCGGGGACAGTGTCCCGCTACGCTCATCACT 71
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Db 1 GCTGCTCCGCGCTCCAGAGCATTCGGGGACAGTGTCCCGCTACGCTCATCACT 60
 |||||||
 72 GACTGCTCATCACTCTTCGCTGCTGCTTCCT 106
 |||||||
Db 61 GACTGCTCATCACTCTTCGCTGCTGCTTCCT 95
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RESULT 12
W1802 214 bp mRNA linear EST 02-OCT-1997
LOCUS mb22202.r1 Soares mouse p3NNP19.5 Mus musculus cDNA clone
DEFINITION IMAGE:330195.5 similar to SW:10X5_RAT P12527 ARACHIDONATE
 5-LIPOXYGENASE ;, mRNA sequence.
VERSION W1802
KEYWORDS W1802.1 GI:1286106
ACCESSION
EST
KEYWORDS house mouse.
SOURCE Mus musculus
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 214)
AUTHORS Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T.,
 Geisler, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M.,
 Scheinberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B.,
 Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and
 Waterston, R.
TITLE The WashU-HMT Mouse EST Project
JOURNAL Unpublished (1996)

COMMENT Contact: Marra M/Mouse EST Project
 WashU-HMT Mouse EST Project
 Washington University School of Medicine
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
 Tel: 314 286 1800
 Fax: 314 286 1810
 Email: mouseest@wustl.edu
 This clone is available royalty-free through LNL; contact the
 IMAGE Consortium (infoimage.lnl.gov) for further information.
 MGI: 211595
 Possible reversed clone: similarity on wrong strand
 Seg primer: mob.REGA+RT
 High quality sequence stop: 177.
FEATURES
 Source
 1..214
 /organism="Mus musculus"
 /db_xref="taxon:10090"
 /clone="IMAGE:330195"
 /clone_lib="Soares mouse p3NNP19.5"
 /dev_stage="19.5 dpc total fetus"
 /lab_host="DH10B (ampicillin resistant)"
 /note="Vector: pRT73D (Pharmacia) with a modified
 polylinker; Site 1: Not I; Site 2: Eco RI; 1st strand cDNA
 was primed with a Not I - oligo(dT) primer [5'
 TGTACCAATCTGACAGTGGAGGCGGCGGCTTTTCTTTTCTTTT 3']
 double-stranded cDNA was size selected, ligated to Eco RI
 adapters (Pharmacia), digested with Not I and cloned into
 the Not I and Eco RI sites of a modified pRT73 vector
 (Pharmacia). Library went through one round of
 normalization to a Cot = 5. Library constructed by Benito
 Soares and M.Fatima Bonaldo. RNA was kindly provided by
 Dr. Minoru Ko (Wayne State University)."

BASE COUNT 46 a 53 c 68 g 47 t
ORIGIN

Query Match 23.6%; Score 89.8; DB 10; Length 214;
 Best Local Similarity 97.1%; Pred. No. 6.7e-16;
 Matches 102; Conservative 0; Mismatches 2; Indels 1; Gaps 1;

QY 272 CGGGGTCAGAGCTGCTGCTGATTTTCGATGATGACAGCTGGCGTGTGACGC 331
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Db 1 CGGGGTCAGAGCTGCTGCTGATTTTCGATGATGACAGCTGGCGTGTGACGC 60
 |||||||
 332 GATGAGAGGAGTGCATGATCATCATCATATATATACCAA 376
 |||||||
Db 61 GATGAGAGGAGTGCATGAC AGAGATCATCATATATATACCAA 104
 |||||||

RESULT 13
BB587762 214 bp mRNA linear EST 30-NOV-2000
LOCUS BB587762 RIKEN full-length enriched, adult female vagina Mus
DEFINITION musculus cDNA clone 9930104L01.5, mRNA sequence.
VERSION BB587762.1 GI:11484306
KEYWORDS EST.
ACCESSION
EST
KEYWORDS house mouse.
SOURCE Mus musculus
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 214)
AUTHORS Aizawa, K., Akahira, S., Akimura, T., Arai, A., Arakawa, T., Carninci, P.,
 Hanagaki, T., Hayatsu, N., Hirooka, T., Hirozane, T., Hodojima, Y.,
 Imotani, K., Ishii, Y., Itoh, M., Izawa, M., Kawai, J., Kojima, Y., Kono
 H., Kusakabe, M., Matsuyama, T., Miyazaki, A., Nakamura, M., Nishii, K.,
 Nomura, K., Numazaki, R., Okazaki, Y., Okido, T., Owa, C., Sakai, C.,
 Sakai, K., Sasaki, D., Sato, K., Shibata, K., Shibata, Y., Shinagawa, A.,
 Shiraki, T., Sogabe, Y., Suzuki, H., Tagawa, A., Takahashi, F., Tanaka
 T., Toya, T., Watahiki, A., Yamamura, T., Yasunishi, A., Yoshida, K.,
 Yoshiki, A., Muramatsu, M. and Hayashizaki, Y.
TITLE RIKEN Mouse ESTs (Aizawa, K. et al. 2000)
JOURNAL Unpublished (2000)

COMMENT

Contact: Yoshinide Hayashizaki
Laboratory for Genome Exploration Research Group, RIKEN Genomic
Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
Tel: 81-45-503-9222
Fax: 81-45-503-9216
Email: genome-res@gsc.riken.go.jp,
URL: http://genome.gsc.riken.go.jp/

Carninci, P., Nishiyama, Y., Westover, A., Itoh, M., Nagaoka, S., Sasaki, N., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
Thermotabilization and thermoeactivation of thermostable enzymes by trehalose and its application for the synthesis of full length cDNA. Proc. Natl. Acad. Sci. U.S.A. 95 (2), 520-524 (1998)
Itoh, M., Katsunai, T., Akiyama, J., Shibata, K., Izawa, M., Kawai, J., Tomaru, Y., Carninci, P., Shibata, Y., Ozawa, Y., Muramatsu, M., Okazaki, Y. and Hayashizaki, Y.
Automated filtration-based high-throughput plasmid preparation system. Genome Res. 9 (5), 463-470 (1999)
Carninci, P. and Hayashizaki, Y.
High-efficiency full-length cDNA cloning. Methods Enzymol. 303, 19-44 (1999)
Please visit our web site (http://genome.rtc.riken.go.jp) for further details.

FEATURES

Source

1. .214
/organism="Mus musculus"
/db_xref="taxon:10090"
/clone="930104L01"
/clone_1lb="RIKEN full-length enriched, adult female vagina"
/sex="female"
/tissue_type="vagina"
/dev_stage="adult"
/lab_host="DH10B"
/note="Site-1: Saili; Site-2: BamHI; cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN, Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. 1st strand cDNA was primed with a primer [5' GAGAGAGAGATCCAGACGCTCTTTTCTTTTCTTNN 3']. cDNA was prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length by cap-trapper. cDNA went through one round of normalization to Rot - 10.0 and subtraction to Rot = 185.0. Second strand cDNA was prepared with the primer adapter of sequence [5' GAGAGAGATTCGAGTTATTTAATATATCCCCCCCC 3']. cDNA was cleaved with XhoI and BamHI. Vector: a modified pBluescript KS(+) after bulk excision from Lambda PLC I."

BASE COUNT 48 a 57 c 52 g 57 t
ORIGIN

Query Match

Best Local Similarity 23.2%; Score 88; DB 9; Length 214;
Matches 94; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

QY 3 AAGCAGACAGCTGCTCCGGCTCCAGAGCATTCGCGGACATGGTCCCGCTGACTGC 62
Db 6 AGGCAACAAGCTGCTCCGGGTCCAAAGCATTCGCGGAAATGGTCCCGCTGATGC 65
QY 63 TCCATCACTGACTGCTCATCATCTCTTCTGCTGCTTCCCT 106
Db 66 TCCATCACTGATGCTCATCATCTCTTCCCTTGGCTTCCCT 109

RESULT 14 257 bp mRNA linear EST 28-AUG-1996
AA038641
LOCUS
DEFINITION m194a06.r1 Soares mouse p3JNM19.5 Mus musculus cDNA clone

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

IMAGE:474226.5' similar to SW:LOX5_RAT P12527 ARACHIDONATE
5-LIPOXYGENASE ;, mRNA sequence.
AA038641
AA038641.1 GI:1514164

REFERENCE
AUTHORS

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mus musculus
house mouse.
EST.
1 (bases 1 to 257)
Marta, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T.,
Giesel, S., Kuwaba, T., Lacy, M., Le, M., Martin, J., Morris, M.,
Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B.,
Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and
Waterston, R.

TITLE
JOURNAL
COMMENT

The WashU-HM1 Mouse EST Project
Unpublished (1996)
Contact: Marta M/Mouse EST Project
WashU-HM1 Mouse EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: mouseest@wustl.edu
This clone is available royalty-free through LNL; contact the
IMAGE Consortium (info@image.lnl.gov) for further information.
MGI:284970
Possible reversed clone: similarity on wrong strand
Seq primer: -28M13 rev2 from Amerham
High quality sequence stop: 219.

FEATURES

Source

1. .257
/organism="Mus musculus"
/db_xref="taxon:10090"
/clone="IMAGE:474226"
/clone_1lb="Soares mouse p3JNM19.5"
/dev_stage="19.5 dpc total fetus"
/lab_host="DH10B (ampicillin resistant)"
/note="Vector: pT73D (Pharmacia) with a modified polylinker; Site-1: Not I; Site-2: Eco RI; 1st strand cDNA was primed with a Not I - 0190(dR) primer [5' TGTACCAATCTGAGATGAGGAGGCGGCTTTTCTTTTCTTNN 3']. double-stranded cDNA was size selected, ligated to Eco RI adapters (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of a modified pT73 vector (Pharmacia). Library went through one round of normalization to a Cot = 5. Library constructed by Bento Soares and M. Fatima Bonaldo. RNA was kindly provided by Dr. Minoru Ko (Wayne State University)."

BASE COUNT 59 a 64 c 75 g 59 t
ORIGIN

Query Match

Best Local Similarity 21.2%; Score 80.4; DB 9; Length 257;
Matches 92; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

QY 283 ACCGCTGGGATATTATTCGATGACAGCTGCGGTGTGATCGGATGAGAGCT 342
Db 1 ACCGCTGGGATATTATTCGATGACAGCTGCGGTGTGATCGGATGAGAGCT 60
QY 343 ACGTACTAGAGATCATCATATTATTATTAACCAA 376
Db 61 ACGTATC-AGAGATCATCATATTATTATTAACCAA 93

RESULT 15 449 bp mRNA linear EST 27-JAN-1999
A1385442
LOCUS
DEFINITION m194a06.y1 Soares mouse p3JNM19.5 Mus musculus cDNA clone
IMAGE:474226.5' similar to TR:O15296 O15296 15S-LIPOXYGENASE. ;,
mRNA sequence.
ACCESSION A1385442

VERSION AI365442.1 GI:4198905

KEYWORDS EST.

SOURCE house mouse.

ORGANISM Mus musculus

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 449)

AUTHORS Marra,M., Hillier,L., Kucaba,T., Martin,J., Beck,C., Wylie,T., Underwood,K., Steptoe,M., Theising,B., Allen,M., Bowers,Y., Person,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurk,R., Ritter,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann,R., Waterston,R. and Wilson,R.

TITLE The Mashu-NCI Mouse EST Project 1999

JOURNAL Unpublished (1999)

COMMENT Contact: Marra M/Mashu-NCI Mouse EST Project 1999
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810
Email: mouseest@watson.wustl.edu

This clone is available royalty-free through LNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
MG1:284970
This read is a RESEQUENCE of a previously sequenced mouse clone correct orientation)
This read has been verified (found to hit its original self in the possible reversed clone: similarity on wrong strand
Seq primer: -40RP from Glibco
High quality sequence stop: 418.

FEATURES

source

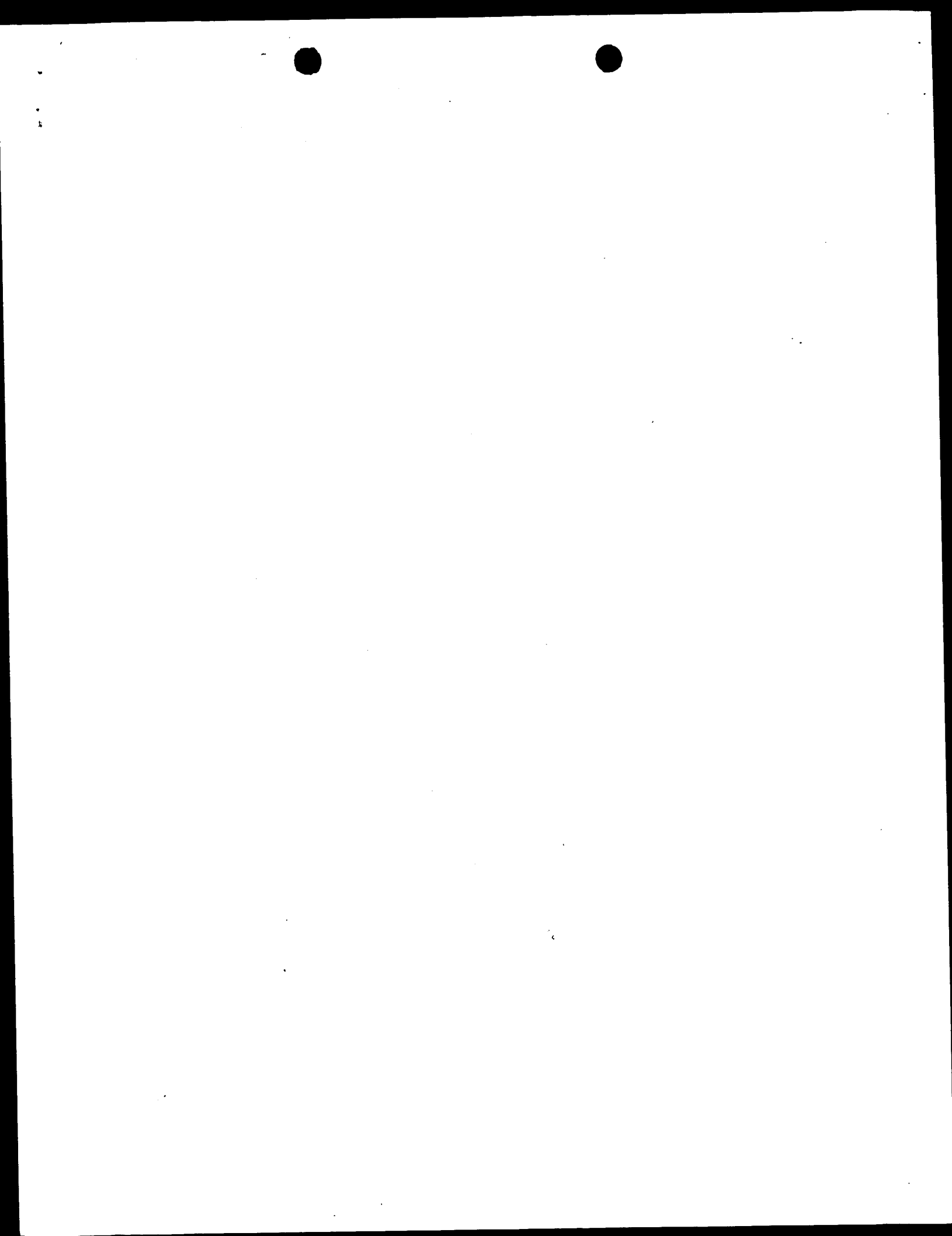
Location/Qualifiers
1..449
/organism="Mus musculus"
/db_xref="taxon:10090"
/clone="IMAGE:474226"
/clone_id="Soares mouse p3NMF19.5"
/dev_stage="19.5 dpc total fetus"
/lab_host="DH10B (ampicillin resistant)"
/note="Vector: pT73D (Pharmacia) with a modified polylinker: Site 1: Not I; Site 2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer [5', TGTTACCAATCTGAAGTGGAGCGGCCGATTTTCTTTTCTTTT 3'], double-stranded cDNA was size selected, ligated to Eco RI adapters (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of a modified pT73 vector (Pharmacia). Library went through one round of normalization to a Cot = 5. Library constructed by Bento Soares and M.Fatima Bonaldo. RNA was kindly provided by Dr. Minoru Ko (Wayne State University)."

GC COUNT 104 a 123 c 122 g 100 t

Query Match 21.2%; Score 80.4; DB 9; Length 449;
Best Local Similarity 97.9%; Pred.No.5.4e-13;
Matches 92; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

QY 283 ACCTGCTGGGTATTTCCGATGACAGCGCTGCTGTACGCGATGAGAGGT 342
DB 1 ACCTGCTGGGTATTTCCGATGACAGCGCTGCTGTACGCGATGAGAGGT 60
QY 343 ACCTGCTGAGATCATCTATTTATACCAAA 376
DB 61 ACCTGAC-AGAGTCACTTATTTATACCAA 93

Search completed: May 25, 2002, 00:50:47
Job time: 24294 sec



GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: May 24, 2002, 18:53:03 ; Search time 62.9 seconds
(without alignments)
1483.954 Million cell updates/sec

Title: W36511

Perfect score: 380
Sequence: 1 GCAGGACGACGCTGCTGCC.....ACTTATTATTACCAATGAC 380

Scoring table: IDENTITY_NUC
Gapop 10.0, Gapext 1.0

Number of hits satisfying chosen parameters: 767066

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 08
Maximum Match 1008
Listing first 45 summaries

Database :

Issued Patents: NA:
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2: /cgn2_6/ptodata/1/ina/5B.COMB.seq:*
3: /cgn2_6/ptodata/1/ina/6A.COMB.seq:*
4: /cgn2_6/ptodata/1/ina/6B.COMB.seq:*
5: /cgn2_6/ptodata/1/ina/PCFUS.COMB.seq:*
6: /cgn2_6/ptodata/1/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description
1	135.8	35.7	2469	3	US-09-087-727-1
2	50	13.2	2685	4	US-09-061-768A-1
3	50	13.2	3205	4	US-09-061-768A-3
4	33.4	8.8	2124	4	US-09-198-122-1
5	33.2	8.7	20235	1	US-07-642-734C-3
6	33.2	8.7	20235	3	US-08-439-009A-3
7	32.4	8.5	2049	4	US-09-099-749-10
8	30.8	8.1	3271	2	US-08-852-806-1
9	30.8	8.1	3271	2	US-09-163-669-1
10	30	7.9	3710	4	US-07-741-453A-62
11	29.8	7.8	2297	1	US-08-484-493-1
12	29.8	7.8	2297	1	US-08-484-494-1
13	29.8	7.8	2297	2	US-08-345-212-1
14	29.8	7.8	2297	2	US-09-249-003-1
15	29.8	7.8	3357	3	US-08-726-214-7
16	29.4	7.7	1598	1	US-08-211-682-34
17	29	7.6	441529	4	US-09-103-840A-1
18	28.8	7.6	586	1	US-08-385-590A-3
19	28.8	7.6	586	1	US-09-021-520-3
20	28.8	7.6	31571	1	US-08-323-443B-1
21	28.8	7.6	53526	3	US-08-658-136-2
22	28.8	7.6	53577	3	US-08-658-136-1
23	28.4	7.5	2968	4	US-09-813-819-1
24	28.4	7.5	2968	4	US-09-920-048-1
25	28.4	7.5	49377	1	US-08-764-233A-1
26	28	7.4	1225	2	US-08-829-110-4
27	28	7.4	28958	1	US-08-258-261B-6

C 28	28	7.4	28958	1	US-08-456-837-6	Sequence 6, Appli
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C 31	28	7.4	28958	1	US-08-458-076A-6	Sequence 6, Appli
C 32	28	7.4	28958	1	US-08-457-335A-6	Sequence 6, Appli
C 33	28	7.4	28958	1	US-08-457-335A-6	Sequence 6, Appli
C 34	28	7.4	28958	1	US-08-729-214-6	Sequence 6, Appli
C 35	28	7.4	28958	3	US-09-028-934-6	Sequence 6, Appli
36	27.8	7.3	198	2	US-08-588-258B-22	Sequence 22, Appli
37	27.8	7.3	198	5	US-08-460-505-22	Sequence 22, Appli
38	27.8	7.3	198	5	PCT-US96-08295-22	Sequence 22, Appli
39	27.6	7.3	2291	2	US-08-476-062A-53	Sequence 53, Appli
40	27.4	7.2	1945	1	US-08-724-194-1	Sequence 1, Appli
41	27.4	7.2	2678	1	US-08-724-194-2	Sequence 2, Appli
42	27.4	7.2	3933	1	US-08-199-776-1	Sequence 1, Appli
43	27.4	7.2	3933	3	US-08-663-731-1	Sequence 1, Appli
44	27.4	7.2	3933	3	US-08-879-338-1	Sequence 1, Appli
45	27.4	7.2	3933	5	PCT-US95-02044-1	Sequence 1, Appli

ALIGNMENTS

RESULT 1
US-09-087-727-1
; Sequence 1, Application US/09087727A
; Patent No. 6103496
; GENERAL INFORMATION:
; APPLICANT: Brash, Alan R
; APPLICANT: Boeglin, William E
; APPLICANT: Kim, Richard B
; TITLE OF INVENTION: Isolated and Purified 12R-Lipoxygenase Protein and
; FILE REFERENCE: Attorney Docket No. 6103496 1242-7
; CURRENT APPLICATION NUMBER: US/09/087,727A
; CURRENT FILING DATE: 1998-05-29
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: Patentln Ver. 2.0
; SEQ ID NO 1
; LENGTH: 2469
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (260)..(2362)
US-09-087-727-1

Query Match 35.7%; Score 135.8; DB 3; Length 2469;
Best Local Similarity 83.4%; Pred. No. 4.2e-36;
Matches 166; Conservative 0; Mismatches 32; Indels 1; Gaps 1;

QY 175 TTTCCTGGGCTTACAGGCTTCCACAGTGATGCTTCCGCTCTGAGCTACT 234
DB 1626 TGTCCCTGGGCTTACAGGCTTCCACAGTGATGCTTCCGCTCTGAGCTACT 1685
QY 235 ACAAGCCTTCCATTCACAGCTTTTGAGAGCGGCTCCAGAGCTCGCTGGT 294
DB 1686 ATGACGCTCTACTCTCCCAATGACTTGTGGGCTGAGGCTGAGGCTGAGG 1745
QY 295 ATATTCCTGATGACAGCTTGGGCTGTGTCAGGATGAGAGCTAGCTAGAG 354
DB 1746 ATTACTACCTCGATGACAGCTTGTGCTGAGGCTGAGGCTGAGGCTGAGG 1804
QY 355 ATCATCTATTATTATTC 373
DB 1805 ATCATCTATTATTATTC 1823

RESULT 2
US-09-061-768A-1
; Sequence 1, Application US/09061768A
; Patent No. 6204037

GENERAL INFORMATION:
APPLICANT: BRASH, ALAN R.
APPLICANT: BOEGLIN, WILLIAM E.
APPLICANT: JISAKA, MITSUO
TITLE OF INVENTION: LIPOXYGENASE PROTEINS AND NUCLEIC ACIDS
NUMBER OF SEQUENCES: 36
CORRESPONDENCE ADDRESS:
ADDRESSEE: ARLES A. TAYLOR, JR.
STREET: SUITE 1400, UNIVERSITY TOWER, 3100 TOWER BOULEVARD
CITY: DURHAM
STATE: NORTH CAROLINA
COUNTRY: USA
ZIP: 27707
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4 MB storage
COMPUTER: IBM PC/XT/AT compatible
OPERATING SYSTEM: Windows 3.1
SOFTWARE: WORD PERFECT 6.1 and ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/061,768A
FILING DATE: APRIL 16, 1998
CLASSIFICATION: 435
PRIOR APPLICATION DATA: NONE
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: ARLES A. TAYLOR, JR.
REGISTRATION NUMBER: 39,395
REFERENCE/DOCKET NUMBER: 1242/5
TELECOMMUNICATION INFORMATION:
TELEPHONE: (919) 493-8000
TELEFAX: (919) 419-0383
TELEX:
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2685 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: unknown
US-09-061-768A-1

Query Match 13.2%; Score 50; DB 4; Length 2685;
Best Local Similarity 56.6%; Pred. No. 4.4e-07;
Matches 112; Conservative 0; Mismatches 85; Indels 1; Gaps 1;

QY 179 CCTGGGCTAGAGGCTTCGACAGATGATGTTCCGGGCTGCTGAGCTACCTACCA 238
DB 1367 CATGGGATTGAAGGCTTCTGAGTTGATACAGAGACATGAAGCCTGAACCTATTC 1426
DB 239 AAGCCTCTGATTCACAGACTTTGTGAGCGCGGGGTCACAGACCTGCCCTGGATTA 298
DB 1427 TCTCTGTGTCTGCTGAGATATCCGACCCGAGAGTTGAAGACATCCACAGCTACFA 1486
QY 299 TTTCCGATGACAGCCTGGCGGTGTGTACCGGATGGAAGTACGTACTGAGATCA 358
DB 1487 CTACCGATGATGAGGATGAGATTGGGGTGAGTGGAACGCTTGTCTCT-CAATCA 1545
QY 359 TCACCTATTATTACCAAA 376
DB 1546 TCGGTATCTACTACCA 1563

RESULT 3
US-09-061-768A-3
Sequence 3, Application US/09061768A
GENERAL INFORMATION:
APPLICANT: BRASH, ALAN R.
APPLICANT: BOEGLIN, WILLIAM E.
APPLICANT: JISAKA, MITSUO
TITLE OF INVENTION: LIPOXYGENASE PROTEINS AND NUCLEIC ACIDS
NUMBER OF SEQUENCES: 36

CORRESPONDENCE ADDRESS:
ADDRESSEE: ARLES A. TAYLOR, JR.
STREET: SUITE 1400, UNIVERSITY TOWER, 3100 TOWER BOULEVARD
CITY: DURHAM
STATE: NORTH CAROLINA
COUNTRY: USA
ZIP: 27707
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4 MB storage
COMPUTER: IBM PC/XT/AT compatible
OPERATING SYSTEM: Windows 3.1
SOFTWARE: WORD PERFECT 6.1 and ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/061,768A
FILING DATE: APRIL 16, 1998
CLASSIFICATION: 435
PRIOR APPLICATION DATA: NONE
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: ARLES A. TAYLOR, JR.
REGISTRATION NUMBER: 39,395
REFERENCE/DOCKET NUMBER: 1242/5
TELECOMMUNICATION INFORMATION:
TELEPHONE: (919) 493-8000
TELEFAX: (919) 419-0383
TELEX:
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 3205 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: unknown
US-09-061-768A-3

Query Match 13.2%; Score 50; DB 4; Length 3205;
Best Local Similarity 53.0%; Pred. No. 4.8e-07;
Matches 107; Conservative 0; Mismatches 95; Indels 0; Gaps 0;

QY 179 CCTGGGCTAGAGGCTTCGACAGATGATGTTCCGGGCTGCTGAGCTACCTACCA 238
DB 1299 CTTGGACACTGGGGATTTCTGACCTGATTAAGAGAAATGAGAGCTGAACCTACTC 1358
QY 239 AAGCCTCTGATTCACAGACTTTGTGAGCGCGGGGTCACAGACCTGCCCTGGATTA 298
DB 1359 TGTCTGTGTCTCTGCTGAGATATCCGACCCGAGAGTGTGGAAGCATCCAGGCTACTA 1418
QY 299 TTTCCGATGACAGCCTGGCGGTGTGTACCGGATGGAAGTACGTACTGAGATCA 358
DB 1419 TTACGAGATGATGGGATGACAGATCTGGGGGCAATTAAGAGCTTGTCTGAAATAGT 1478
QY 359 TCACCTATTATTACCAATGAC 380
DB 1479 CAGCATCTACTATCCAAAGTGAC 1500

RESULT 4
US-09-198-122-1
Sequence 1, Application US/09198122
Patent No. 6180380
GENERAL INFORMATION:
APPLICANT: Strebhardt, Klaus; Rubsamen-Waligmann, Helga;
APPLICANT: Holtrich, Uwe
TITLE OF INVENTION: CLONING OF A MEMBER OF THE SERINE-
TITLE OF INVENTION: THREONINE-KINASE FAMILY
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSEE: SPRUNG HORN KRAMER & WOODS
STREET: 660 White Plains Road
CITY: Tarrytown
STATE: New York
COUNTRY: U.S.A.

ZIP: 10591-5144
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 2.0 MB
MEDIUM TYPE: storage
COMPUTER: NEC Powermate SX-20
OPERATING SYSTEM: DOS
SOFTWARE: WordPerfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/198,122
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/601,014
FILING DATE: 23-FEB-1996
APPLICATION NUMBER: PCT/JP94/02863
FILING DATE: 30-AUG-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DE 4329177
FILING DATE: 30-AUG-1993
ATTORNEY/AGENT INFORMATION:
NAME: Kurt G. Briscoe
REGISTRATION NUMBER: 33,141
REFERENCE/DOCKET NUMBER: Bayer 9516-KGB
TELECOMMUNICATION INFORMATION:
TELEPHONE: (914) 332-1700
TELEFAX: (914) 332-1844
TELEX:
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2124 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: linear
MOLECULE TYPE: cDNA
ANTI-SENSE: yes
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: 65..1873
US-09-198-122-1

Query Match 8.8%; Score 33.4; DB 4; Length 2124;
Best Local Similarity 58.6%; Pred. No. 0.16;
Matches 58; Conservative 0; Mismatches 41; Indels 0; Gaps 0;

225 GAGCTACCTACGAAAGCCCTCTGATCCCAAGACTTTGTGGAGCGGGGTCCAGGAC 284
1268 GATCTGCTGCTGATCCCTCTGATCCCAAGACTTTGTGGAGCGGGGTCCAGGAC 1327

285 CTGCTGGGTATATTTCCGTGATGACAGCGCGGGGTG 323
1328 GGCCTTGGTATCAAGCTCTGTGTATACAGCGGTGGGGTG 1366

RESULT 5
US-07-642-734C-3/C
Sequence 3, Application US/07642734C
Patent No. 5824513
GENERAL INFORMATION:
APPLICANT: Katz, L
APPLICANT: Donadio, S
APPLICANT: McAlpine, J B
TITLE OF INVENTION: Recombinant DNA Method for Producing
TITLE OF INVENTION: Erythromycin Analogs
NUMBER OF SEQUENCES: 27
CORRESPONDENCE ADDRESS:
ADDRESSEE: Edward H. Gorman
STREET: Abbott Laboratories D377/AP6D-2 One Abbott
CITY: Abbott Park
STATE: IL

COUNTRY: US
ZIP: 60064-3500
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/642,734C
FILING DATE: 17-JAN-91
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Danckerts, Andreas M
REGISTRATION NUMBER: 32652
REFERENCE/DOCKET NUMBER: 4952.US.01
TELECOMMUNICATION INFORMATION:
TELEPHONE: 708-937-9396
TELEFAX: 708-938-2623
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 20235 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: unknown
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Saccharopolyspora erythraea
STRAIN: NRRL 238
FEATURE:
NAME/KEY: CDS
LOCATION: 19..10722
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OTHER INFORMATION: 6-deoxyerythronolide B"
FEATURE:
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LOCATION: 19..4470
OTHER INFORMATION: /function="approximate span of
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NAME/KEY: misc_feature
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OTHER INFORMATION: /product="orf3 encoding modules 5 & 6
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NAME/KEY: misc_feature
LOCATION: 10831..12174
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LOCATION: 12379..13350
OTHER INFORMATION: /function="approximate span of
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NAME/KEY: misc_feature
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LOCATION: 18379..18921
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OTHER INFORMATION: beta-ketoreductase domain of module 6"
FEATURE:
NAME/KEY: misc_feature

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LOCATION: 19149..19398
OTHER INFORMATION: /function="approximate span of
OTHER INFORMATION: acyl carrier domain of module 6"
FEATURE:
NAME/KEY: misc_feature
LOCATION: 19492..20235
OTHER INFORMATION: /function="approximate span of
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US-07-642-734C-3

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Query Match      8.7%; Score 33.2; DB 1; Length 20235;
Best Local Similarity 52.1%; Pred. No. 0.59;
Matches 74; Conservative 0; Mismatches 68; Indels 0; Gaps 0;

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QY 189 GAGGCTTCGACAGCTATGTTGGGGCTGCTGTAGCTACCTACAAAGCCTCTGC 248
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DB 17682 GAGCTCGGCGATCAGTCTCTCCGCGGTGCGGTCAGCAGCAGCCGATGCCAGGC 17623
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QY 249 ATTCCCAACGACTTGTGAGCGCGGGGTCCAGACCTGCTGGGTATTTTCGTGAT 308
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DB 17622 GTCCCGGCGGATCTCTGACCGCGCGGTGAGCAGCAGCGGTGCGGTATCTGAGGAA 17563
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QY 309 GACAGCTGGCGGTGTGTACG 330
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RESULT 6
US-08-439-009A-3/c
; Sequence 3, Application US/08439009A
; Patent No. 6004787
; GENERAL INFORMATION:
; APPLICANT: Donadio, S
; APPLICANT: Katz, L
; TITLE OF INVENTION: Method of Directing Biosynthesis of
; TITLE OF INVENTION: Specific Polypeptides
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Steven F. Weinstock
; STREET: Abbott Laboratories D377/APD-2 One Abbott
; CITY: Abbott Park
; STATE: IL
; COUNTRY: US
; ZIP: 60064-3500
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/439,009A
; FILING DATE: 11-MAY-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Casuto, Dianne
; REGISTRATION NUMBER: 40,943
; REFERENCE/DOCKET NUMBER: 4952.US.D1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 847-938-3137
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20235 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: unknown
; MOLECULE TYPE: DNA (genomic)
; HYPOTHEICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Saccharopolyspora erythraea

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STRAIN: NRRL 238
FEATURE:
NAME/KEY: CDS
LOCATION: 19..10722
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OTHER INFORMATION: /function="gene eryA"
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OTHER INFORMATION: 6-deoxyerythronolide B"
FEATURE:
NAME/KEY: misc_feature
LOCATION: 19..4470
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OTHER INFORMATION: module 3"
FEATURE:
NAME/KEY: misc_feature
LOCATION: 97..1482
OTHER INFORMATION: /function="approximate span of
OTHER INFORMATION: beta-ketoacyl ACP synthase of module 3"
FEATURE:
NAME/KEY: misc_feature
LOCATION: 1693..2670
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OTHER INFORMATION: acyltransferase domain module 3"
FEATURE:
NAME/KEY: misc_feature
LOCATION: 3406..3921
OTHER INFORMATION: /function="approximate span of
OTHER INFORMATION: beta-ketoreductase domain of module 3"
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NAME/KEY: misc_feature
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FEATURE:
NAME/KEY: misc_feature
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OTHER INFORMATION: module 4"
FEATURE:
NAME/KEY: misc_feature
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FEATURE:
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OTHER INFORMATION: /function="approximate span of
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FEATURE:
NAME/KEY: misc_feature
LOCATION: 9433..9984
OTHER INFORMATION: /function="approximate span
OTHER INFORMATION: beta-ketoreductase of module 4"
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LOCATION: 10225..10483
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OTHER INFORMATION: acyl carrier domain of module 4"
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LOCATION: 10723..15165

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OTHER INFORMATION: /function="approximate span of
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NAME/KEY: misc_feature
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OTHER INFORMATION: beta-ketoreductase of module 5"
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NAME/KEY: misc_feature
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LOCATION: 15172..16569
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LOCATION: 18379..18921
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NAME/KEY: misc_feature
LOCATION: 19149..19398
OTHER INFORMATION: /function="approximate span of
OTHER INFORMATION: acyl carrier domain of module 6"
FEATURE:
NAME/KEY: misc_feature
LOCATION: 19492..20235
OTHER INFORMATION: /function="approximate span of
OTHER INFORMATION: thioesterase domain of module 6"
US-08-439-009A-3

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Query Match      8.7%; Score 33.2; DB 3; Length 20235;
Best Local Similarity 52.1%; Pred. No. 0.59;
Matches 74; Conservative 0; Mismatches 66; Indels 0; Gaps 0;

QY 189 GAGGCTTCGACAGGTGATGTTGGGGTCTGCTGACCTCCTACAAAAGCCTCTGC 248
DB 17682 GAGCTGGGCGATGAGTGTCTCCGCGGTGTCGCGGTGACGACCGGATGGCAGCGC 17623

QY 249 ATCCCAAGCACTTGTGGAGCGGCGGTCGAGACGCGCTGGTATTATTTCCGTGAT 308
DB 17622 GTCCGGGGGAGATCTCTGACCGCGCGGTGAGCACGCGGTGCGGGCTCATCTGAGGAA 17563

QY 309 GACAGCTTGGCGGTGTGTAACG 330
DB 17562 GGTGGCTGACCGTGGCGACG 17541

RESULT 7

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US-09-099-749-10
; Sequence 10, Application US/09099749B
; Patent No. 6306591
; GENERAL INFORMATION:
; APPLICANT: Utah State University
; TITLE OF INVENTION: Screening For The Molecular Defect Causing Spider Lamb
; FILE REFERENCE: 370605
; CURRENT APPLICATION NUMBER: US/09/099,749B
; CURRENT FILING DATE: 1998-06-18
; EARLIER APPLICATION NUMBER: 60/050,127
; EARLIER FILING DATE: 1997-06-18
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: Corel WordPerfect 8.0
; SEQ ID NO 10
; LENGTH: 2049
; TYPE: DNA
; ORGANISM: Sheep
US-09-099-749-10

Query Match 8.5%; Score 32.4; DB 4; Length 2049;
Best Local Similarity 55.3%; Pred. No. 0.34; Mismatches 0; Gaps 0;
Matches 63; Conservative 0; Indels 51; Gaps 0;

QY 226 AGCTACCTACCAAGACCTGTCATTCCTCCAGACATTGTTGGAGCGCGGCTCCAGAGCC 285
DB 1383 agctaccttcaagacctgtgtctcgtaccagtgctgctgagtgatgagatc 1442
QY 286 TGCCGTGGATTATTTCCGTGATGACAGCCGTGGCGGTGTGTAGCGATGGAGA 339
DB 1443 tggcctcgagagatgcatcctagagacctgctgagcccgacagctgctgtga 1496

RESULT 8
US-08-852-806-1/c
; Sequence 1, Application US/08852806
; Patent No. 5874245
; GENERAL INFORMATION:
; APPLICANT: Shoji Fukusumi
; APPLICANT: Shuji Hinuma
; TITLE OF INVENTION: NOVEL HUMAN G-PROTEIN COUPLED RECEPTOR
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Smithkline Beecham Corporation
; STREET: 709 Swedeland Road
; CITY: King of Prussia
; STATE: PA
; COUNTRY: U.S.A.
; ZIP: 19406-0939
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FASTSEQ Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/852,806
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/017,915
; FILING DATE: 16 MAY 1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Han, William T
; REGISTRATION NUMBER: 34,344
; REFERENCE/DOCKET NUMBER: TAK50002
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 610-270-5219
; TELEFAX: 610-270-5090
; TELEX:
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3271 base pairs

TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE:
ORIGINAL SOURCE:
US-08-852-806-1

Query Match 8.1%; Score 30.8; DB 2; Length 3271;
Best Local Similarity 66.7%; Pred. No. 1.5;
Matches 44; Conservative 0; Mismatches 22; Indels 0; Gaps 0;

QY 4 AGGACGAGCTGCTCCCGCTCCAGAGCATTGCGGAGACAGTGTCCGCTGACTGCT 63
DB 239 AGACAGCGCGCGCTGGCAGACCTTGAGCATTGCGGAGCATTGTGTAGATGATCTCG 180
QY 64 CCATCA 69
DB 179 CCAGCA 174

RESULT 9
US-09-163-669-1/c
; Sequence 1, Application US/09163669
; Patent No. 611076
; GENERAL INFORMATION:
; APPLICANT: FUKUSUMI, SHOJI
; APPLICANT: FUJII, RYO
; APPLICANT: HINUMA, SHUJI
; TITLE OF INVENTION: NOVEL HUMAN G-PROTEIN COUPLED
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Ratner & Prestlia
; STREET: P.O. Box 980
; CITY: Valley Forge
; STATE: PA
; COUNTRY: USA
; ZIP: 19482
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FASTSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/163,669
; FILING DATE: 30-SEP-1998
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/852,806
; FILING DATE: 07-MAY-1997
; APPLICATION NUMBER: 60/017,915
; FILING DATE: 16-MAY-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Prestlia, Paul F
; REGISTRATION NUMBER: 23,031
; REFERENCE/DOCKET NUMBER: TAK-50002-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 610-407-0700
; TELEFAX: 610-407-0700
; TELEX: 846169
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3271 base pairs
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; TOPOLOGY: linear
; MOLECULE TYPE: CDNA
US-09-163-669-1

Query Match 8.1%; Score 30.8; DB 3; Length 3271;
Best Local Similarity 66.7%; Pred. No. 1.5;
Matches 44; Conservative 0; Mismatches 22; Indels 0; Gaps 0;

QY 4 AGGAGAGCGTGGCCCGGCTCCAGAGGACATTCGCGGAGAGTTCCTCCGCTGACTGCT 63
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QY 64 CCATCA 69
DB 179 CCAGCA 174

- RESULT 10 -

US-07-741-453A-62
Sequence 62, Application US/07741453A
Patent No. 6228597

GENERAL INFORMATION:

APPLICANT: PARMENTIER, MARC
APPLICANT: LIBERT, FREDERIC
APPLICANT: DIMONT, JACQUES
APPLICANT: VASSART, GILBERT
TITLE OF INVENTION: POLYPEPTIDES HAVING THYROTROPIN-RECEPTOR
TITLE OF INVENTION: ACTIVITY, NUCLEIC ACID SEQUENCES CODING FOR SUCH RECEPTORS
TITLE OF INVENTION: AND POLYPEPTIDES, AND APPLICATIONS OF THESE POLYPEPTIDES
NUMBER OF SEQUENCES: 62
CORRESPONDENCE ADDRESS:

ADDRESSEE: CUSHMAN DARBY & CUSHMAN
STREET: 1615 L STREET, N.W.
CITY: WASHINGTON, D.C.
COUNTRY: U.S.A.
ZIP: 20036

COMPUTER READABLE FORM:

MEDIUM TYPE: Disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/741.453A
FILING DATE: 19911015
CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: KOKULIS, PAUL N.
REGISTRATION NUMBER: 16773
REFERENCE/DOCKET NUMBER: 91913/1107/US/ST
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 861-3000
TELEFAX: (202) 822-0944

INFORMATION FOR SEQ ID NO:

62:
SEQUENCE CHARACTERISTICS:
LENGTH: 3710 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
US-07-741-453A-62

Query Match 7.9%; Score 30; DB 4; Length 3710;
Best Local Similarity 49.4%; Pred. No. 3;
Matches 78; Conservative 0; Mismatches 80; Indels 0; Gaps 0;

QY 46 TGGTCCCGCTGAGCTGCTCCATCATGACTGCTCATCATCTGCTGCTGCTGCTGCTCC 105
DB 126 TGGCTTCCTCCCTCGGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 185
QY 106 TGGTCCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 165
DB 186 TTTCTCCACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 245
QY 166 TAAGAAATATTTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 203

DB 246 CTTGAATGTGTTCTCTCTCCCGAGGCGAGAGCTGAG 283

RESULT 11

US-08-484-493-1
Sequence 1, Application US/08484493
Patent No. 5728381

GENERAL INFORMATION:

APPLICANT: Wilson, Peter J
APPLICANT: Morris, Charles P
APPLICANT: Anson, Donald S
APPLICANT: Occhiodoro, Teresa
APPLICANT: Bielecki, Julie
APPLICANT: Clements, Peter R
APPLICANT: Hopwood, John J
TITLE OF INVENTION: GLYCOSYLATION VARIANTS OF
TITLE OF INVENTION: IDURONATE 2-SULFATASE
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:

ADDRESSEE: Scully, Scott, Murphy & Presser
STREET: 400 Garden City Plaza
CITY: Garden City
STATE: New York
COUNTRY: USA
ZIP: 11530

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/484.493
FILING DATE: 07-JUN-1995
CLASSIFICATION: 424

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 991,973
FILING DATE: 17-DEC-1992
ATTORNEY/AGENT INFORMATION:
NAME: Digilio, Frank S
REGISTRATION NUMBER: 31,346
REFERENCE/DOCKET NUMBER: 84162
TELECOMMUNICATION INFORMATION:
TELEPHONE: 516-742-4343
TELEFAX: 516-742-4366
TELEX: 230 901 SANS UR
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:

LENGTH: 2297 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 125..1774
US-08-484-493-1

Query Match 7.8%; Score 29.8; DB 1; Length 2297;
Best Local Similarity 51.1%; Pred. No. 2.8;
Matches 70; Conservative 0; Mismatches 67; Indels 0; Gaps 0;

QY 177 TCCCTGGGCGCTAGAGGCTTCGACAGAGTGTTCGGGCTGCTGAGCTCAGCTAC 236
DB 272 TCCCTGGGCGCTAGAGGCTTCGACAGAGTGTTCGGGCTGCTGAGCTCAGCTAC 331
QY 237 AAAGGCTTCGATTCCTCCAGAGCTTTGTGAGCGCGGCTCCAGAGAGCTGCTGGGTAT 296
DB 332 CACAGCCTCTCTCCAGAGATGCTTTGGCAGCAAGCAGTGTGGCGCCGAGCGGCTT 391
QY 297 TATTTCCGTGATGACAG 313

Db 392 TCCTTCTCACTGGCAG 408

RESULT 12

US-08-484-494-1

; Sequence 1, Application US/08484494
; Patent No. 5798239
; GENERAL INFORMATION:
; APPLICANT: Wilson, Peter J
; APPLICANT: Morris, Charles P
; APPLICANT: Anson, Donald S
; APPLICANT: Occhiodoro, Teresa
; APPLICANT: Bielicki, Julie
; APPLICANT: Clements, Peter R
; APPLICANT: Hopwood, John J
; TITLE OF INVENTION: GLYCOSYLATION VARIANTS OF
; TITLE OF INVENTION: IDURONATE 2-SULFATASE
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Scully, Scott, Murphy & Presser
; STREET: 400 Garden City Plaza
; CITY: Garden City
; STATE: New York
; COUNTRY: USA
; ZIP: 11530

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/484,494

FILING DATE: 07-JUN-1995

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 991,973

FILING DATE: 17-DEC-1992

ATTORNEY/AGENT INFORMATION:

NAME: Digilio, Frank S

REGISTRATION NUMBER: 31,346

REFERENCE/DOCKET NUMBER: 84162

TELECOMMUNICATION INFORMATION:

TELEPHONE: 516-742-4343

TELEFAX: 516-742-4366

TELEX: 230 901 SANS UR

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 2297 base pairs

TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: linear

MOLECULE TYPE: cDNA

FEATURE:

NAME/KEY: CDS

LOCATION: 125..1774

US-08-484-494-1

Query Match 7.8%; Score 29.8; DB 1; Length 2297;

Best Local Similarity 51.1%; Pred. No. 2.8;

Matches 70; Conservative 0; Mismatches 67; Indels 0; Gaps 0;

Db 177 TCCTTGGGCTTAGAGGCTTCGACAGGTGATGTTGGGGTCTGCTGAGCTCAGCTAC 236

Db 272 TCCTTGGGCTTAGAGGCTTCGACAGGTGATGTTGGGGTCTGCTGAGCTCAGCTAC 331

Qy 237 AAAAGCCTTCGACCTTCCCAAGCACTTGTGAGAGCGCGGGTCCAGAGCTGCTGGAT 296

Db 332 CACAGCCTTCCTTCCAGAAATGCTTGGCGAGCAAGCAAGTGTGCCGCCGAGCCGCTT 391

Qy 297 TATTTCCGTGACAG 313

Db 392 TCCTTCTCACTGGCAG 408

RESULT 13

US-08-345-212-1

; Sequence 1, Application US/08345212
; Patent No. 5932211
; GENERAL INFORMATION:
; APPLICANT: Wilson, Peter J
; APPLICANT: Morris, Charles P
; APPLICANT: Anson, Donald S
; APPLICANT: Occhiodoro, Teresa
; APPLICANT: Bielicki, Julie
; APPLICANT: Clements, Peter R
; APPLICANT: Hopwood, John J
; TITLE OF INVENTION: GLYCOSYLATION VARIANTS OF
; TITLE OF INVENTION: IDURONATE 2-SULFATASE
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Scully, Scott, Murphy & Presser
; STREET: 400 Garden City Plaza
; CITY: Garden City
; STATE: New York
; COUNTRY: USA
; ZIP: 11530

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/345,212

FILING DATE: 07-JUN-1995

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 991,973

FILING DATE: 17-DEC-1992

ATTORNEY/AGENT INFORMATION:

NAME: Digilio, Frank S

REGISTRATION NUMBER: 31,346

REFERENCE/DOCKET NUMBER: 84162

TELECOMMUNICATION INFORMATION:

TELEPHONE: 516-742-4343

TELEFAX: 516-742-4366

TELEX: 230 901 SANS UR

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 2297 base pairs

TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: linear

MOLECULE TYPE: cDNA

FEATURE:

NAME/KEY: CDS

LOCATION: 125..1774

US-08-345-212-1

Query Match 7.8%; Score 29.8; DB 2; Length 2297;

Best Local Similarity 51.1%; Pred. No. 2.8;

Matches 70; Conservative 0; Mismatches 67; Indels 0; Gaps 0;

Db 177 TCCTTGGGCTTAGAGGCTTCGACAGGTGATGTTGGGGTCTGCTGAGCTCAGCTAC 236

Db 272 TCCTTGGGCTTAGAGGCTTCGACAGGTGATGTTGGGGTCTGCTGAGCTCAGCTAC 331

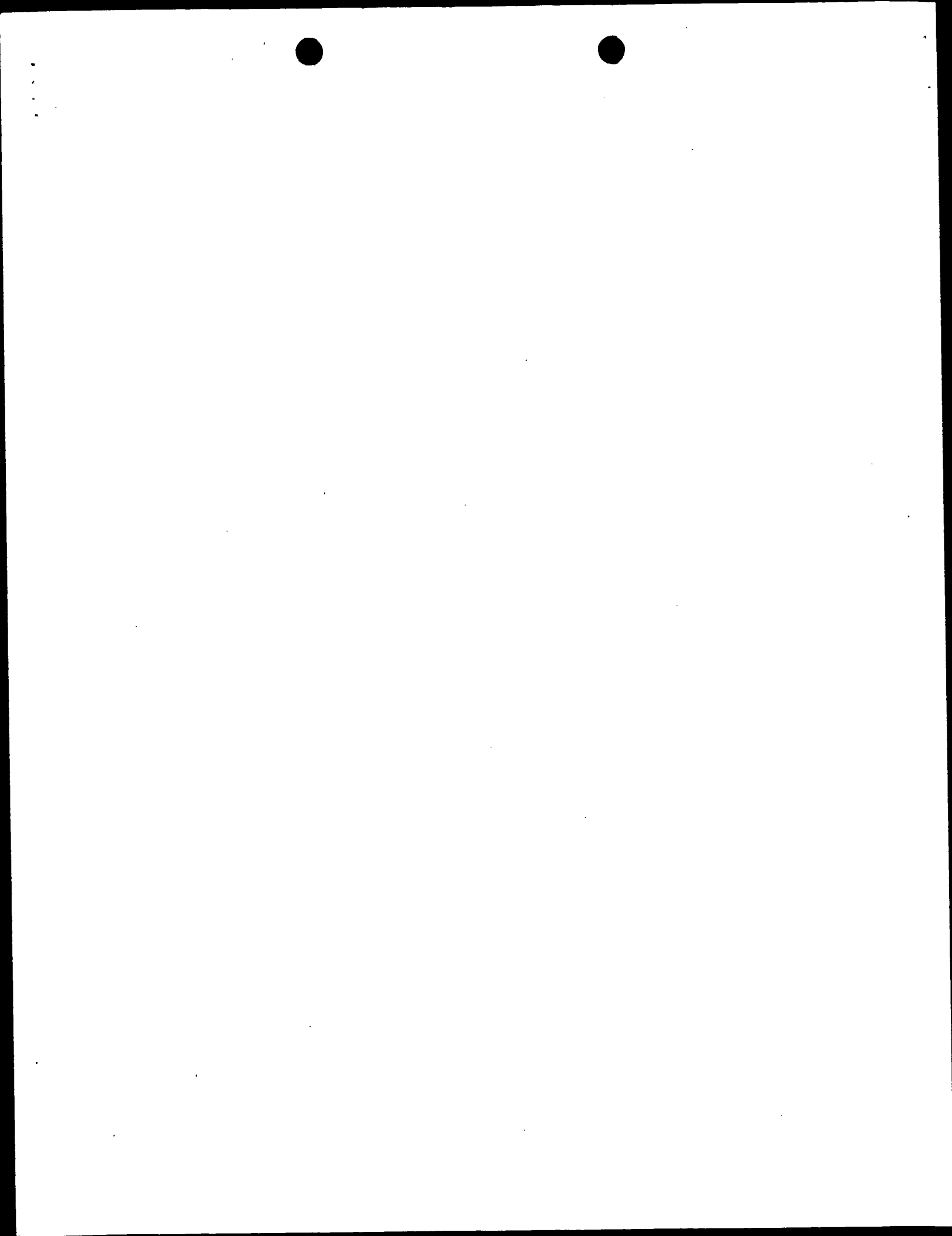
Qy 237 AAAAGCCTTCGACCTTCCCAAGCACTTGTGAGAGCGCGGGTCCAGAGCTGCTGGAT 296

Db 332 CACAGCCTTCCTTCCAGAAATGCTTGGCGAGCAAGCAAGTGTGCCGCCGAGCCGCTT 391

Qy 297 TATTTCCGTGACAG 313

Db 392 TCCTTCTCACTGGCAG 408

322 TCTTCTCTGCTGGCAG 408



XX
XX

Sequence 1383 BP; 296 A; 432 C; 376 G; 279 T; 0 other;

QY 177 TCCCTGGGCGCTAGAGGGCTTCGCAAGAGGATGATGGTTCGGGGTCTGTCTAGCTACCTAC 236

Db 934 tcaatcgagagcgcaaaagggcccatctactccatctaaagcaagcgctctgcaccaattcaactaac 993

QY 237 AAAAGCCTTCGATTCCTCCAAACGACTTTGTGAGACGGGCGGTCCAGGACCTGGCTGGAT 296

Db 994 acaaatcttcgccttcgcagcagcctcgcgggcccgcgcgcttcctgctatccccaactac 1053

QY 297 TATTTCGTATATACAGCCTGCGCGGTGTGTGTAACGGATGAGAGTACGTGATGAGAT 356

Db 1054 cactaacctgaagcagcagcgctcgaagatctctgcygcgcatttgagagcttggctccagaatcc 1113

357 CATCACTTATTATTACCAATGAC 380

1114 gtgggtctaatctatctatcccaagtac 1137

[illegible]

XX	FN		W0200061765-A2.	
XX	PD		19-OCT-2000.	
XX	PF		12-APR-2000; 2000WO-US09657.	
XX	PR	12-APR-1999;	99US-0128817.	
XX	PR	24-AUG-1999;	99US-0150454.	
XX	PA	(LEXI-)	LEXICON GENETICS INC.	
XX	PI	Turner CA,	Zambrowicz B, Nehls M, Friedrich G, Sands AT;	
XX	DR	WPL: 2000-665134/64.		
XX	P-PSDB:	AAB19383.		
PT	Novel polynucleotides encoding human lipoxigenase proteins useful for producing transgenic animals preferably mouse	-		
PS	Claim 1; Page 65-66; 83pp; English.			
CC	AAC61747-60 encode novel human lipoxigenase proteins. Lipoxigenases oxidise lipids to produce leukotrienes. Leukotrienes bind cognate receptors and trigger biological effects. Leukotrienes influence a variety of biological processes, and can serve as, inter alia, potent chemotactic agents and mediators of inflammation, smooth muscle contractions, etc.. Lipoxigenases and leukotrienes are implicated in a variety of diseases and disorders, such as asthma, eye diseases, arthritis, lung disease, cancer, acne, psoriasis, etc..			
SQ	Sequence 1848 BP; 391 A; 568 C; 511 G; 378 T; 0 other:			
	Query Match	14.5%;	Score 55.2;	DB 21; Length 1848;
	Best Local Similarity	54.4%;	Pred. No. 1.2e-07;	
	Matches 111; Conservative	0;	Mismatches 93;	Indels 0; Gaps 0
OY	177 TCCCTGGCGCTAGAGGCGTTCGCACAGGTGATGGTTCCGGGTCGTGACTCACCCTAC	236		
DB	1399 tccatcgaggaggaagcctcatctacccaatgagaacggcgtgcaccactcacctac	1458		
OY	237 AAAAGCCTCTGCATTGCCAACAACATTTGTGTGAACGCGGGGTCAGAACCTGCTGGGTAT	296		
DB	1459 accaatcttcgctccctgcgacgccgcggccgcggcgtcttgcatacccccaactac	1518		
OY	297 TATTTCGGTGATGACAGCCTGGCGGTGTGTGTATGCCCATGACAGTAGAGTAAGTAAAGAT	356		
DB	1519 cactaccgagacgacggcctgaagatcttggygcgatcgagagcctttgctcagaatc	1578		
DB	357 CATCACTTATTATTACCAANTGAC	380		
DB	1579 gtgggctaattatccagtagac	1602		
RESULT	6			
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AAC61749;	AC			
06-MAR-2001	DT	(first entry)		
cDNA encoding a human lipoxigenase protein.	DE			
Human; lipoxigenase; leukotriene; lipid; chemotactic agent; inflammation; smooth muscle contraction; asthma; eye disease; arthritis; lung disease; cancer; acne; psoriasis; ss.	XX			
Homo sapiens.	OS			
key	PH	Location/Qualifiers		
CDS	FT	1..1671		

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FT      /product= "lipoxigenase"
XX
XX      WO200061765-A2.
XX
XX      19-OCT-2000.
XX
XX      12-APR-2000; 2000WO-US09657.
XX
XX      12-APR-1999; 99US-0128817.
XX
XX      24-AUG-1999; 99US-0150454.
XX
XX      (LEXI-) LEXICON GENETICS INC.
XX
XX      Turner CA, Zambrowicz B, Nehls M, Friedrich G, Sands AT;
XX
XX      WPI; 2000-665134/64.
XX
XX      P-PSDB; AAB19381.
XX
XX      Novel polynucleotides encoding human lipoxigenase proteins useful for
XX      producing transgenic animals preferably mouse
XX
XX      Claim 1; Page 62; 83pp; English.
XX
XX      AAC61747-60 encode novel human lipoxigenase proteins. Lipoxigenases
XX      oxidise lipids to produce leukotrienes. Leukotrienes bind cognate
XX      receptors and trigger biological effects. Leukotrienes influence a
XX      variety of biological processes, and can serve as, inter alia, potent
XX      chemotactic agents and mediators of inflammation, smooth muscle
XX      contractions, etc.. Lipoxigenases and leukotrienes are implicated in
XX      a variety of diseases and disorders, such as asthma, eye diseases,
XX      arthritis, lung disease, cancer, acne, psoriasis, etc..
XX
XX      Sequence 2236 BP; 493 A; 733 C; 555 G; 455 T; 0 other;
XX
XX      Query Match      14.5%; Score 55.2; DB 21; Length 2236;
XX      Best Local Similarity 54.4%; Pred. No. 1.3e-07;
XX      Matches 111; Conservative 0; Mismatches 93; Indels 0; Gaps
XX
XX      177 TCCCTGGCGCTAGAGGCTTCGCACAGGTGATGGTGGGGGTGTCGTGAGCTACCTAC 236
XX      111 111 111 111 111 111 111 111 111 111 111 111 111 111 111
XX      934 tccatcggaagcaagagccctatactatactatgtgcacgagcctgcgcacctcactac 993
XX
XX      237 AAAAGCCTTCGATTCGCCAACGACTTTGTGGAGCGCGGGGTCCAGACCTGCCTGGGTAT 296
XX      111 111 111 111 111 111 111 111 111 111 111 111 111 111
XX      994 accaatctctgcctccgcagacgcctgcggccgcgcgcctgcctacccccactac 1053
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XX      297 TATTTCCGATGACACAGCCTGGCGGTGTGTAACGGATGGAGGTACGTGACTAGAGAT 356
XX      111 111 111 111 111 111 111 111 111 111 111 111 111 111
XX      1054 cactaccagagacagcgccctgaagatcccgcgccatgtagaagcttgctcagaatc 1113
XX
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XX      11 11 11 11 1111
XX      1114 gtggctactattatccacgtgac 1137
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XX      Db
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XX      RESULT      7
XX      AAC61760
XX      ID AAC61760 standard; cDNA; 2316 BP.
XX
XX      AAC61760.
XX
XX      06-MAR-2001 (first entry)
XX
XX      cDNA encoding a human lipoxigenase protein.
XX
XX      Human; lipoxigenase; leukotriene; lipid; chemotactic agent;
XX      inflammation; smooth muscle contraction; asthma; eye disease; arthritis;
XX      lung disease; cancer; acne; psoriasis; ss.
XX
XX      Homo sapiens.
XX

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Key Location/Qualifiers
 CDS 1..2316
 /*tag= a
 /product= "lipoxigenase"

W0200061765-A2.

19-OCT-2000.

12-APR-2000; 2000MO-US09657.

12-APR-1999; 99US-0128817.

24-AUG-1999; 99US-0150454.

(LEXI-) LEXICON GENETICS INC.

Turner CA, Zambrowicz B, Nehls M, Friedrich G, Sands AT;

WPI: 2000-665134/64.

P-PSDB; AAB19392.

Novel polynucleotides encoding human lipoxigenase proteins useful for producing transgenic animals preferably mouse
 Claim 1; Page 79; 83pp; English.

AAC61747-60 encode novel human lipoxigenase proteins. Lipoxigenases oxidise lipids to produce leukotrienes. Leukotrienes bind cognate receptors and trigger biological effects. Leukotrienes influence a variety of biological processes, and can serve as, inter alia, potent chemotactic agents and mediators of inflammation, smooth muscle contractions, etc.. Lipoxigenases and leukotrienes are implicated in a variety of diseases and disorders, such as asthma, eye diseases, arthritis, lung disease, cancer, acne, psoriasis, etc..

Sequence 2316 BP; 486 A; 724 C; 651 G; 455 T; 0 other;

Query Match 14.5%; Score 55.2; DB 21; Length 2316;
 Best Local Similarity 54.4%; Pred. No. 1.3e-07;
 Matches 111; Conservative 0; Mismatches 93; Indels 0; Gaps 0;

QY 177 TCCCTGGGCTTAGAGGCTTCGACAGGTGATGGTTCGGGTCTGTGAGCTCACCTAC 236
 1867 tccatcggaagcaagagcctcatctacatgacagcgccggtccacttccactac 1926
 237 AAAAGCCTCTGATCCCAAGACTTTGTGAGCGCGGGTCCAGACCTGGGTAT 296
 1927 accatttctgcttcgagacagcctgagccgagcggtccgtatccccaactac 1986
 QY 297 TATTTCCGTGATGACAGCCTTGCGGTGTGATCGGATGAGAGGTACGTAGAGAT 356
 1987 cactaccgagagcagcgagcctgagatctggcgagccatgagagcttgcctcagaatc 2046
 QY 357 CATCACTTATTTATCCCAATGAC 380
 2047 gtgggctactatattccagtgac 2070

RESULT 8
 AAC61758
 ID AAC61758 standard; cDNA; 2604 BP.

XX AAC61758;

XX 06-MAR-2001 (first entry)

XX cDNA encoding a human lipoxigenase protein.

XX Human; lipoxigenase; leukotriene; lipid; chemotactic agent;
 XX inflammation; smooth muscle contraction; asthma; eye disease; arthritis;
 KW lung disease; cancer; acne; psoriasis; ss.

Homo sapiens.
 Key Location/Qualifiers
 CDS 1..2604
 /*tag= a
 /product= "lipoxigenase"

W0200061765-A2.

19-OCT-2000.

12-APR-2000; 2000MO-US09657.

12-APR-1999; 99US-0128817.

24-AUG-1999; 99US-0150454.

(LEXI-) LEXICON GENETICS INC.

Turner CA, Zambrowicz B, Nehls M, Friedrich G, Sands AT;

WPI: 2000-665134/64.

P-PSDB; AAB19390.

Novel polynucleotides encoding human lipoxigenase proteins useful for producing transgenic animals preferably mouse
 Claim 1; Page 73-74; 83pp; English.

AAC61747-60 encode novel human lipoxigenase proteins. Lipoxigenases oxidise lipids to produce leukotrienes. Leukotrienes bind cognate receptors and trigger biological effects. Leukotrienes influence a variety of biological processes, and can serve as, inter alia, potent chemotactic agents and mediators of inflammation, smooth muscle contractions, etc.. Lipoxigenases and leukotrienes are implicated in a variety of diseases and disorders, such as asthma, eye diseases, arthritis, lung disease, cancer, acne, psoriasis, etc..

Sequence 2604 BP; 554 A; 840 C; 709 G; 501 T; 0 other;

Query Match 14.5%; Score 55.2; DB 21; Length 2604;
 Best Local Similarity 54.4%; Pred. No. 1.4e-07;
 Matches 111; Conservative 0; Mismatches 93; Indels 0; Gaps 0;

QY 177 TCCCTGGGCTTAGAGGCTTCGACAGGTGATGGTTCGGGTCTGTGAGCTCACCTAC 236
 1867 tccatcggaagcaagagcctcatctacatgacagcgccggtccacttccactac 1926
 237 AAAAGCCTCTGATCCCAAGACTTTGTGAGCGCGGGTCCAGACCTGGGTAT 296
 1927 accatttctgcttcgagacagcctgagccgagcggtccgtatccccaactac 1986
 QY 297 TATTTCCGTGATGACAGCCTTGCGGTGTGATCGGATGAGAGGTACGTAGAGAT 356
 1987 cactaccgagagcagcgagcctgagatctggcgagccatgagagcttgcctcagaatc 2046
 QY 357 CATCACTTATTTATCCCAATGAC 380
 2047 gtgggctactatattccagtgac 2070

RESULT 9
 AAC61747
 ID AAC61747 standard; cDNA; 2701 BP.

XX AAC61747;

XX 06-MAR-2001 (first entry)

XX cDNA encoding a human lipoxigenase protein.

XX Human; lipoxigenase; leukotriene; lipid; chemotactic agent;
 XX inflammation; smooth muscle contraction; asthma; eye disease; arthritis;
 KW lung disease; cancer; acne; psoriasis; ss.

KW lung disease; cancer; acne; psoriasis; ss.
 OS Homo sapiens.
 XX Key location/Qualifiers
 XX FT 1..2136
 XX CDS /tag= a
 FT /product= "lipoxygenase"
 XX
 PN
 XX WO20061765-A2.
 PD 19-OCT-2000.
 XX 12-APR-2000; 2000WO-US09657.
 PF 12-APR-1999; 99US-0128817.
 PR 24-AUG-1999; 99US-0150454.
 XX
 PA (LEXI-) LEXICON GENETICS INC.
 PI Turner CA, Zambrowicz B, Nehls M, Friedrich G, Sands AT;
 DR WPI; 2000-665134/64.
 PT P-PSDB: AAB19379.
 PT Novel polynucleotides encoding human lipoxygenase proteins useful for
 PS producing transgenic animals preferably mouse
 PS Claim 1: Page 57-58; 83pp; English.
 XX
 XX AHC61747-60 encode novel human lipoxygenase proteins. Lipoxygenases
 CC oxidise lipids to produce leukotrienes. Leukotrienes bind cognate
 CC receptors and trigger biological effects. Leukotrienes influence a
 CC variety of biological processes, and can serve as, inter alia, potent
 CC chemotactic agents and mediators of inflammation, smooth muscle
 CC contractions, etc.. Lipoxygenases and leukotrienes are implicated in
 CC a variety of diseases and disorders, such as asthma, eye diseases,
 CC arthritis, lung disease, cancer, acne, psoriasis, etc..
 XX
 XX Sequence 2701 BP; 588 A; 869 C; 690 G; 554 T; 0 other;
 SO
 Query Match 14.5%; Score 55.2; DB 21; Length 2701;
 Best Local Similarity 54.4%; Pred. No. 1.4e-07;
 Matches 111; Conservative 0; Mismatches 93; Indels 0; Gaps 0
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 Db 1399 tccatcggaagcagcagccttactctactctatgcagcagcgcccttccacttccact 1458
 237 AAAAGCTCTGCATTCACACGACTTCTGAGCGGGGCGGACGACCTGCGGGTAT 296
 Db 1459 accaatctctcctccgcgacagcagcctgcggccgcgcgcgcctcgtctalccccaactac 1518
 Oy 297 TATTTCCGTGATGACAGCGCTGCGGTGTGTACCGCATGTGAGAGTACGTACGAT 356
 Db 1519 cactaccgagacgacgagcctgaagatctggcgccatltgagagccttgcctcagaatc 1578
 Oy 357 CATCACTTATTATTACCAATGAC 380
 Db 1579 gtggcctactatattcccaagtac 1602
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 ID ABA05868
 ID ABA05868 standard; CDNA; 3320 BP.
 XX ABA05868;
 AC
 XX 21-MAR-2002 (first entry)
 DT
 XX Human lipoxygenase 46638 coding sequence.
 DE
 XX

KW	Human; lipoxigenase; 46638; cytosolic; antiarrhythmic; hypotensive;
KW	antiatherosclerotic; cardiant; vasotropic; hypertensive;
KW	antiinflammatory; neuroprotective; nootropic; antiparinsonian;
KW	anticonvulsant; hepatotropic; dermatological; antispasmodic; fungicide;
KW	antidiarrheic; antitumor; antidiabetic; antasthmatic; antiarthritic;
KW	antirheumatic; osteopathic; antihypoid; antiallergic; gene therapy;
KW	ophthalmological; antianemic; analgesic; virucetic;
KW	vulnery; immunomodulator; ss.
XX	
OS	Homo sapiens.
XX	
XX	Key Location/Qualifiers
XX	CD5 459..2594
FT	/*tag= a
FT	/product= "lipoxigenase 46638"
FT	/note= "this region is specifically claimed"
XX	
XX	WO200190323-A2.
PN	
XX	
PD	29-NOV-2001.
XX	
PF	21-MAY-2001: 2001WO-US16380.
XX	
PR	19-MAY-2000: 2000US-205675P.
XX	
PA	(MILL-) MILLENNIUM PHARM INC.
PI	
XX	Meyers RA;
XX	
DR	WPI: 2002-083104/11.
XX	
P	P-PSDB; ABB04578.
XX	
PT	Novel human lipoxigenase family member polypeptide and polynucleotide
PT	for diagnosing, treating immune, blood vessel, cardiovascular,
PT	inflammatory, ovarian, lung, colon, skin disorders and disorders
PT	involving placenta -
XX	
XX	Claim 1: Page 100-102; 118pp: English.
XX	
CC	The present invention provides the protein and coding sequences of a
CC	human protein, which is a member of lipoxigenase family, and is referred
CC	to as 46638. The sequences can be used in the treatment of immune, blood
CC	vessels, cardiovascular, inflammatory, cell differentiation,
CC	neurodegenerative, liver, ovarian, lung, colon, breast, skin disorders,
CC	neurodegenerative, liver, ovarian, lung, colon, breast, skin disorders,
CC	disorders associated with bone metabolism, pain or metabolic disorders,
CC	disorders involving the placenta and viral diseases. The present sequence
CC	is the coding sequence of the invention.
XX	
XX	Sequence 3320 BP; 706 A; 1074 C; 852 G; 683 T; 5 other:
SO	
QY	177 TCCCGGGGCTAGAGGGCTTCGCACAGCTGATGGTTCGGGGCTGTCTGAGCTCACCCTAC 236
DB	1857 tccatcggaaggaagcgctcatctacatctagagcacggcctggccaccatccacctac 1916
QY	237 AAAAGCCTCTGCATTCGCCAAGCACTTTGTGGAGCGGGGGCTGCAGCACTGCTGGGTAT 296
DB	1917 accaatcttcctcctcgcgaagcagcctcggcccgccggcgctcctggatccaccacctac 1976
QY	297 TATTTCGCGATGACAGCGCTGGCGGTGTGTACCGATGAGAGAGTACGTACTAGAGAT 356
DB	1977 cactacgagaaagagcgctgaagatcctggcgccatcttgagagcttgcctcagaatc 2036
QY	357 CATCACTATTATTATACCAAAATGAC 380
DB	2037 gtgggtactactatcatcccaagtac 2060
RESULT	11

[illegible]

RESULT 13

AAD04501 standard; cDNA: 2685 BP.

ID AAD04501;

04-JUL-2001 (first entry)

Human 15S-lipoxygenase (15-Lox-2) cDNA.

Human; 15S-lipoxygenase; 15-Lox-2; non-haeme iron dioxygenase; arachidonic acid; feed additive; livestock; antigen; ss.

Homo sapiens.

Key	Location/Qualifiers
CDS	72..2102
	/tag= a
	/product= "Human 15S-lipoxygenase (15-Lox-2) protein"

US6204037-B1.

20-MAR-2001.

16-APR-1998; 98US-0061768.

16-APR-1998; 98US-0061768.

(UYVA-) UNIV VANDERBILT.

Brash AR, Boeglin WE, Jisaka M;

WPI: 2001-289517/30.

P-PSDB; AAE00935.

New 15S-lipoxygenase nucleic acids and polypeptides, useful as feed additives for livestock, or as antigens for producing antibodies -

Claim 3; Column 43-48; 51pp; English.

The present sequence is human 15S-lipoxygenase (15-Lox-2) cDNA. Lipoxygenases are a structurally related family of non-haeme iron dioxygenases that function in the production of fatty acid hydroperoxides. 15-Lox-2 acts in the metabolism of arachidonic acid to 15-hydro(pero)xyicosatetraenoic acid. Lipoxygenase DNA can be used as diagnostic tools to detect normal and abnormal DNA sequences derived from patient cells, for detecting and isolating other members of the polypeptide family and related polypeptides from a DNA library potentially containing the sequences, as primers for hybridizing to related sequences for amplifying those sequences or for altering native lipoxygenase DNA sequences. The lipoxygenase is useful as feed additives for livestock and as antigens for producing antibodies.

Sequence 2685 BP; 625 A; 829 C; 721 G; 510 T; 0 other;

Query Match 13.2%; Score 50; DB 22; Length 2685;

Best Local Similarity 56.6%; Pred. No. 7.1e-06; Matches 112; Conservative 0; Mismatches 85; Indels 1; Gaps 1;

QY	179	CTTGAGGCTAGAGGCTTCGCACAGTGATGTTGGGGTCTGTCTGACCTGACACCA	238
DB	1367	catcgacatgaagctctctcgtgatacagagaacatgaagcactgacattc	1426
QY	239	AAGCTTCGATTCCTCCAAAGCACTTGTGAGAGCGGGTCCAGGACCTGCTGGATT	298
DB	1427	tctcctggtctcctcgaagataccgacccgagaggttgaagaactccacagctacta	1486
QY	299	TTTCCGTGATGACAGCCTGCGGCTGTGATACGATGAGAGTACCTGACTGACATCA	358
DB	1487	ctacgtagatgagtgcagcagatttggtggtcagtggaacgttctctc-gaaatca	1545

QY 359 TCACCTTATTATTACCAA 376

DB 1546 tcggtatctactaccaca 1563

RESULT 14

AAD04502 standard; cDNA: 3232 BP.

ID AAD04502;

04-JUL-2001 (first entry)

Mouse 8S-lipoxygenase (8-Lox) cDNA.

Mouse; 8S-lipoxygenase; 8-Lox; non-haeme iron dioxygenase; arachidonic acid; feed additive; livestock; antigen; ss.

Mus sp.

Key	Location/Qualifiers
5'UTR	1..27
	/tag= a
CDS	28..2061
	/tag= b
	/product= "Mouse 8S-lipoxygenase (8-Lox) protein"

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16-APR-1998; 98US-0061768.

16-APR-1998; 98US-0061768.

(UYVA-) UNIV VANDERBILT.

Brash AR, Boeglin WE, Jisaka M;

WPI: 2001-289517/30.

P-PSDB; AAE00936.

New 15S-lipoxygenase nucleic acids and polypeptides, useful as feed additives for livestock, or as antigens for producing antibodies -

Example 2; Fig 5A-5C; 51pp; English.

The present sequence is mouse 8S-lipoxygenase (8-Lox) cDNA. Lipoxygenases are a structurally related family of non-haeme iron dioxygenases that function in the production of fatty acid hydroperoxides. 8-Lox acts in the metabolism of arachidonic acid to 8S-hydro(pero)xyicosatetraenoic acid. Lipoxygenase DNA can be used as diagnostic tools to detect normal and abnormal DNA sequences derived from patient cells, for detecting and isolating other members of the polypeptide family and related polypeptides from a DNA library potentially containing the sequences, as primers for hybridizing to related sequences for amplifying those sequences or for altering native lipoxygenase DNA sequences. The lipoxygenase is useful as feed additives for livestock and as antigens for producing antibodies.

Note: The present sequence is also shown in column 51-58 of the specification, but lacks 27 nucleotides at its 5' end.

Sequence 3232 BP; 823 A; 872 C; 782 G; 755 T; 0 other;

Query Match 13.2%; Score 50; DB 22; Length 3232;

Best Local Similarity 53.0%; Pred. No. 7.7e-06; Matches 107; Conservative 0; Mismatches 95; Indels 0; Gaps 0;

QY	179	CTTGAGGCTAGAGGCTTCGCACAGTGATGTTGGGGTCTGTCTGACCTGACACCA	238
DB	1326	ccttgcactgggggactctcgaactgataagaagaacatgagcagctgaactactc	1385

Sequence 2343 BP; 511 A; 688 C; 636 G; 495 T; 13 other;

1480 ctctctaccaragga 1496

Search completed: May 25, 2002, 01:31:09
Job time: 5743 sec

